

SCORE Search Results Details for Application 10663433 and Search Result us-10-663-433- 1.rng.

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This page gives you Search Results detail for the Application 10663433 and Search Result us-10-663-433-1.rng.

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 00:46:44 ; Search time 3886 Seconds
(without alignments)
12519.905 Million cell updates/sec

Title: US-10-663-433-1
Perfect score: 6978
Sequence: 1 atgaagaaaggttctcaaca.....agaatgcctcagccagatga 6978

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6978	100.0	6978	12	ADM06774	Adm06774 Human cen
2	6978	100.0	7433	12	ADQ18630	Adq18630 Human sof
3	6681.2	95.7	7222	8	ACC47248	Acc47248 Human SCA
4	5466.8	78.3	8452	4	AAS59864	Aas59864 Human nov
5	5466.8	78.3	8452	14	AED08238	Aed08238 Human CP1
6	5302.8	76.0	6075	10	ADC30206	Adc30206 Human nov
7	5300.8	76.0	6244	12	ADQ23084	Adq23084 Human sof
8	5034.8	72.2	5902	8	AAL51566	Aal51566 Human nuc
9	3597.4	51.6	3602	13	ADR07863	Adr07863 Full leng
10	3008.6	43.1	3893	15	AEF74782	Aef74782 Human pol
11	2873.6	41.2	3044	11	ADM03364	Adm03364 Human cDN
12	2873.6	41.2	3044	14	AEC86294	Aec86294 Human cDN
13	2403.2	34.4	2631	10	ADB61898	Adb61898 Human cDN
14	1332.8	19.1	1888	4	AAS59821	Aas59821 Human nov
15	1332.8	19.1	1888	14	AED08152	Aed08152 Human CP1
16	922.2	13.2	3048	5	AAS68823	Aas68823 DNA encod
17	912.8	13.1	916	4	AAH99352	Aah99352 Human pro
18	912.8	13.1	916	10	ADC32112	Adc32112 Human nov
19	707.2	10.1	791	2	AAX39736	Aax39736 Gastric c
20	531.8	7.6	667	3	AAA02588	Aaa02588 Human col
21	461.4	6.6	514	2	AAV86265	Aav86265 EST clone
c 22	434.4	6.2	459	4	AAI88234	Aai88234 Human pol
23	427.8	6.1	499	3	AAC79291	Aac79291 Human lun
24	427.8	6.1	499	4	AAD23367	Aad23367 Human lun
25	427.8	6.1	499	10	ADD66641	Add66641 Human lun
26	427.8	6.1	499	10	ADE87895	Ade87895 Human lun
27	373.4	5.4	375	2	AAV36486	Aav36486 Partial n
28	360	5.2	360	5	AAS69956	Aas69956 DNA encod
29	323.4	4.6	442	3	AAC02606	Aac02606 Human sec
30	318.6	4.6	563	12	ACH67011	Ach67011 Human gen
31	316.6	4.5	389	12	ACH80718	Ach80718 Human gen
32	315	4.5	315	2	AAV36481	Aav36481 Partial n
33	314.6	4.5	330	2	AAV36483	Aav36483 Partial n
34	302.6	4.3	784	2	AAZ15475	Aaz15475 Human gen
35	302.6	4.3	784	2	AAX98816	Aax98816 Human val
36	300	4.3	300	2	AAZ14049	Aaz14049 Human gen
37	300	4.3	300	2	AAX98521	Aax98521 Human can
38	284.6	4.1	300	3	AAA01354	Aaa01354 Human col
39	270.8	3.9	541	12	ACH68371	Ach68371 Human gen
40	267	3.8	267	12	ACH82072	Ach82072 Human gen
c 41	261.4	3.7	263	8	ABZ19050	Abz19050 Group III
42	259	3.7	259	6	ABS51581	Abs51581 Human cDN
43	254.8	3.7	295	3	AAA41337	Aaa41337 Human sec
44	229.6	3.3	547	12	ACH68324	Ach68324 Human gen
45	228	3.3	228	2	AAV36487	Aav36487 Partial n

ALIGNMENTS

RESULT 1
ADM06774

ID ADM06774 standard; cDNA; 6978 BP.
 XX
 AC ADM06774;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human centriolin cDNA, SEQ ID NO:1.
 XX
 KW Human; centriolin; centrosome component; cytokinesis; S phase entry;
 KW cell cycle; cell division; cell proliferative disorder; cancer;
 KW leukaemia; psoriasis; Hodgkin's disease; lymphoma; myelofibrosis;
 KW polycythemia vera; cytostatic; antipsoriatic; antisense gene therapy;
 KW chromosome 9q34.11-34.13; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .6978
 FT /*tag= a
 FT /product= "Centriolin"
 XX
 PN WO2004024887-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 15-SEP-2003; 2003WO-US028985.
 XX
 PR 13-SEP-2002; 2002US-0410520P.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Doxsey SJ;
 XX
 DR WPI; 2004-329475/30.
 DR P-PSDB; ADM06775.
 DR GENBANK; AF513978.
 XX
 PT New centrosome nucleic acid molecules, useful for treating cancer,
 PT leukemia, psoriasis, Hodgkin's disease, lymphoma, myelofibrosis,
 PT polycythemia vera, or another cell proliferative disorder.
 XX
 PS Claim 1; SEQ ID NO 1; 107pp; English.
 XX
 CC The invention relates to human centriolin (ADM06775) and nucleic acids
 CC encoding it (ADM06774). Centriolin and pericentrin-B are both core
 CC centrosome components required for progression through cytokinesis and
 CC entry into the S phase of the cell cycle. The invention also relates to a
 CC method of reducing cell division by administering to a cell a centriolin-
 CC or pericentrin-B modulator (particularly a RNAi (interfering RNA), siRNA
 CC (short interfering RNA), antisense nucleic acid, ribozyme or antibody)
 CC effective to disrupt microtubule organisation; and a method of treating
 CC abnormal centrosome function in a cell by administering to the cell an
 CC amount of centriolin or pericentrin-B effective to restore normal
 CC centrosome function. The nucleic acid molecules and methods are useful
 CC for treating cancer, leukaemia, psoriasis, Hodgkin's disease, lymphoma,
 CC myelofibrosis, polycythemia vera, or other cell proliferative disorders.
 CC The present sequence represents cDNA encoding human centriolin.
 XX
 SQ Sequence 6978 BP; 2552 A; 1330 C; 1672 G; 1424 T; 0 U; 0 Other;

Query Match 100.0%; Score 6978; DB 12; Length 6978;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 6978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC	60
Db	1	ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC	60
Qy	61	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTCACCTTTGATTGGA	120
Db	61	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTCACCTTTGATTGGA	120
Qy	121	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	180
Db	121	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	180
Qy	181	GAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT	240
Db	181	GAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT	240
Qy	241	AGATATATTACAGAGGCCCTCATTAATAAACTTACTAAACAGGATAATTTGGCTTTGATA	300
Db	241	AGATATATTACAGAGGCCCTCATTAATAAACTTACTAAACAGGATAATTTGGCTTTGATA	300
Qy	301	AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	360
Db	301	AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	360
Qy	361	TTGGAAAAATGTGTTAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	420
Db	361	TTGGAAAAATGTGTTAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	420
Qy	421	GAAAAGTTGGACAAGCTGTTAAAAATTACGTGAAGTCAACTTATCATATAACAAAATCAGC	480
Db	421	GAAAAGTTGGACAAGCTGTTAAAAATTACGTGAAGTCAACTTATCATATAACAAAATCAGC	480
Qy	481	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	540
Db	481	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	540
Qy	541	ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	600
Db	541	ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	600
Qy	601	AAAGGCAACAAGATATCATCGTCCAAGATATAAGCAAGTTGAAACCGCTTCAAGATTTG	660
Db	601	AAAGGCAACAAGATATCATCGTCCAAGATATAAGCAAGTTGAAACCGCTTCAAGATTTG	660
Qy	661	ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC	720
Db	661	ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC	720
Qy	721	ATTTTCCACCTCCGTTTATTGGAAAGTTTGAAGGTCAGCCAGTAACCACTCAGGATAGA	780
Db	721	ATTTTCCACCTCCGTTTATTGGAAAGTTTGAAGGTCAGCCAGTAACCACTCAGGATAGA	780
Qy	781	CAGGAGGCTTTTGAGAGATTCACTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA	840
Db	781	CAGGAGGCTTTTGAGAGATTCACTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA	840
Qy	841	AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTTCCTTGAGGAAATT	900

Db	841	AAAAAGATGATAGAAACTGAAGAGCTTAAGAGCAAAACAAACAAGGTTTCCTTGAGGAAATT	900
Qy	901	AAAAATCAAGATAAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC	960
Db	901	AAAAATCAAGATAAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC	960
Qy	961	TGTGAGGAACTCAAGAGTGA CTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA	1020
Db	961	TGTGAGGAACTCAAGAGTGA CTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA	1020
Qy	1021	GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA	1080
Db	1021	GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA	1080
Qy	1081	ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA	1140
Db	1081	ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA	1140
Qy	1141	GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA	1200
Db	1141	GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA	1200
Qy	1201	GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1260
Db	1201	GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1260
Qy	1261	CAACTTAGAAATGATCACATGAACCTTGAGAGGCCACACACCACTGGACACGCAACTGGAA	1320
Db	1261	CAACTTAGAAATGATCACATGAACCTTGAGAGGCCACACACCACTGGACACGCAACTGGAA	1320
Qy	1321	GACAAAGAAAAAAAAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATA	1380
Db	1321	GACAAAGAAAAAAAAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATA	1380
Qy	1381	GAAAAGGCAGAACAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACTGGAAGAAGCT	1440
Db	1381	GAAAAGGCAGAACAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACTGGAAGAAGCT	1440
Qy	1441	ATACAACTAAAAAAGATTTT CAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGT	1500
Db	1441	ATACAACTAAAAAAGATTTT CAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGT	1500
Qy	1501	AGACTACAACCTTGTAATAAAATTACGCCAGGAAGCTCTGGATCTAGA ACTGCAGATGGAA	1560
Db	1501	AGACTACAACCTTGTAATAAAATTACGCCAGGAAGCTCTGGATCTAGA ACTGCAGATGGAA	1560
Qy	1561	AAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATA	1620
Db	1561	AAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATA	1620
Qy	1621	GATAGCTTGGATTCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAAGAGCGGTAAA	1680
Db	1621	GATAGCTTGGATTCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAAGAGCGGTAAA	1680
Qy	1681	GAACAACAGCTTGACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAG	1740
Db	1681	GAACAACAGCTTGACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAG	1740
Qy	1741	ATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACT	1800
Db	1741	ATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACT	1800

Qy	1801	GAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGG	1860
Db	1801	GAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGG	1860
Qy	1861	TTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGG	1920
Db	1861	TTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGG	1920
Qy	1921	AAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	1980
Db	1921	AAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	1980
Qy	1981	GACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTCAGAGCTA	2040
Db	1981	GACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTCAGAGCTA	2040
Qy	2041	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2100
Db	2041	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2100
Qy	2101	CTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2160
Db	2101	CTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2160
Qy	2161	CAGCTCAAGGAAGAGTTGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2220
Db	2161	CAGCTCAAGGAAGAGTTGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2220
Qy	2221	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCAGTTC	2280
Db	2221	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCAGTTC	2280
Qy	2281	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGAT	2340
Db	2281	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGAT	2340
Qy	2341	GACAATAATCTGTTAAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2400
Db	2341	GACAATAATCTGTTAAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2400
Qy	2401	GATGGTTTGGTTCGTCCAGAAGAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGT	2460
Db	2401	GATGGTTTGGTTCGTCCAGAAGAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGT	2460
Qy	2461	AAATTAGGAAGTGGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2520
Db	2461	AAATTAGGAAGTGGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2520
Qy	2521	GCTGATTTACAGAAACAATTTCAGTGAAATTCCTGACGCTCCAAGTGGGAAAGAGATGAA	2580
Db	2521	GCTGATTTACAGAAACAATTTCAGTGAAATTCCTGACGCTCCAAGTGGGAAAGAGATGAA	2580
Qy	2581	GCACAAGTTAGAGAGAGAAAACTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAGTGGCA	2640
Db	2581	GCACAAGTTAGAGAGAGAAAACTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAGTGGCA	2640
Qy	2641	ACTGGACAAGAAGAGTTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2700
Db	2641	ACTGGACAAGAAGAGTTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2700

Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATATTTGCAA	2760
Db	2701		
Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATATTTGCAA	2760
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCCTTACAGATCTCCAACCTCAGGAAGCT	2820
Db	2761		
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCCTTACAGATCTCCAACCTCAGGAAGCT	2820
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Db	2821		
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAAGTGAAGAACTAAAG	2940
Db	2881		
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAAGTGAAGAACTAAAG	2940
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Db	2941		
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Qy	3001	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	3001		
Qy	3001	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Qy	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Db	3061		
Qy	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Db	3121		
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3240
Db	3181		
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3240
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3300
Db	3241		
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3300
Qy	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3360
Db	3301		
Qy	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3360
Qy	3361	CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGA	3420
Db	3361		
Qy	3361	CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGA	3420
Qy	3421	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAAGTTTCAGCCATAGTTCCAG	3480
Db	3421		
Qy	3421	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAAGTTTCAGCCATAGTTCCAG	3480
Qy	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3540
Db	3481		
Qy	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3540
Qy	3541	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600
Db	3541		
Qy	3541	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600
Qy	3601	GTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3660

Db	3601	 GTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3660
Qy	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCT	3720
Db	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCT	3720
Qy	3721	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCCTGTACCCAGGGCATG	3780
Db	3721	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCCTGTACCCAGGGCATG	3780
Qy	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
Db	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
Qy	3841	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCATGGTGTATGGGCCTCCACCCCCAAC	3900
Db	3841	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCATGGTGTATGGGCCTCCACCCCCAAC	3900
Qy	3901	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3960
Db	3901	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3960
Qy	3961	TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4020
Db	3961	TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4020
Qy	4021	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4080
Db	4021	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4080
Qy	4081	CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4140
Db	4081	CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4140
Qy	4141	CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4200
Db	4141	CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4200
Qy	4201	CTTATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4260
Db	4201	CTTATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4260
Qy	4261	ATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGA	4320
Db	4261	ATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGA	4320
Qy	4321	CTCCTGGCAGAGGCTGAGAGTGAACCTTTCATGCACTAAAGAAAAGACAAAAATGCTGTT	4380
Db	4321	CTCCTGGCAGAGGCTGAGAGTGAACCTTTCATGCACTAAAGAAAAGACAAAAATGCTGTT	4380
Qy	4381	GAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTA	4440
Db	4381	GAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTA	4440
Qy	4441	GAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4500
Db	4441	GAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4500
Qy	4501	CTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAA	4560

Db	4501	CTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAA	4560
Qy	4561	GAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAG	4620
Db	4561	GAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAG	4620
Qy	4621	GAAAAACTGACAGAAGAGCTTCAGAACTACAGAAAGACATAGAGATGGCAGAACGCAAT	4680
Db	4621	GAAAAACTGACAGAAGAGCTTCAGAACTACAGAAAGACATAGAGATGGCAGAACGCAAT	4680
Qy	4681	GAGGATCACCACCTGCAGGTCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCC	4740
Db	4681	GAGGATCACCACCTGCAGGTCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCC	4740
Qy	4741	GAGCTGGAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGAC	4800
Db	4741	GAGCTGGAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGAC	4800
Qy	4801	AGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCA	4860
Db	4801	AGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCA	4860
Qy	4861	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAAGTGAAGTGAAT	4920
Db	4861	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAAGTGAAGTGAAT	4920
Qy	4921	CACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	4980
Db	4921	CACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	4980
Qy	4981	GTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAG	5040
Db	4981	GTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAG	5040
Qy	5041	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5100
Db	5041	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5100
Qy	5101	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5160
Db	5101	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5160
Qy	5161	CAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTA	5220
Db	5161	CAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTA	5220
Qy	5221	GAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTC	5280
Db	5221	GAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTC	5280
Qy	5281	CTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCAGCTTTACAATCG	5340
Db	5281	CTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCAGCTTTACAATCG	5340
Qy	5341	TGTGTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAA	5400
Db	5341	TGTGTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAA	5400
Qy	5401	AAAAAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAG	5460
Db	5401	AAAAAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAG	5460

Qy	5461	CAATCAAACCTTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAACTAGACCAA	5520
Db	5461	CAATCAAACCTTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAACTAGACCAA	5520
Qy	5521	CTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAA	5580
Db	5521	CTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAA	5580
Qy	5581	GAAAAACGAGAAGCAGTAAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTG	5640
Db	5581	GAAAAACGAGAAGCAGTAAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTG	5640
Qy	5641	AACCTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAG	5700
Db	5641	AACCTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAG	5700
Qy	5701	CAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAA	5760
Db	5701	CAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAA	5760
Qy	5761	GAAGAGGAGACAAAAACAACAACCTTCAAGTGCTTCAGAATGAGATTGAAGAAAAACAAG	5820
Db	5761	GAAGAGGAGACAAAAACAACAACCTTCAAGTGCTTCAGAATGAGATTGAAGAAAAACAAG	5820
Qy	5821	CTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAA	5880
Db	5821	CTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAA	5880
Qy	5881	GAAAGCAAATTAGAAAACAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAG	5940
Db	5881	GAAAGCAAATTAGAAAACAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAG	5940
Qy	5941	GAATTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAA	6000
Db	5941	GAATTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAA	6000
Qy	6001	GAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTC	6060
Db	6001	GAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTC	6060
Qy	6061	TCCCAAACCTAAACGGCAGCTTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAG	6120
Db	6061	TCCCAAACCTAAACGGCAGCTTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAG	6120
Qy	6121	CTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAAC	6180
Db	6121	CTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAAC	6180
Qy	6181	CAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTT	6240
Db	6181	CAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTT	6240
Qy	6241	AAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGC	6300
Db	6241	AAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGC	6300
Qy	6301	ATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCATGAGCGGGCCAGG	6360
Db	6301	ATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCATGAGCGGGCCAGG	6360

Qy	6361	CGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATG	6420
Db	6361	CGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATG	6420
Qy	6421	GCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTT	6480
Db	6421	GCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTT	6480
Qy	6481	AAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6540
Db	6481	AAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6540
Qy	6541	GAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTG	6600
Db	6541	GAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTG	6600
Qy	6601	GAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAAACTG	6660
Db	6601	GAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAAACTG	6660
Qy	6661	AACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAA	6720
Db	6661	AACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAA	6720
Qy	6721	CTGCGTCACCGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCA	6780
Db	6721	CTGCGTCACCGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCA	6780
Qy	6781	GAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAA	6840
Db	6781	GAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAA	6840
Qy	6841	GTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCGTCATCACCCAGT	6900
Db	6841	GTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCGTCATCACCCAGT	6900
Qy	6901	CTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAG	6960
Db	6901	CTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAG	6960
Qy	6961	AATGCCTCAGCCAGATGA	6978
Db	6961	AATGCCTCAGCCAGATGA	6978

RESULT 2

ADQ18630

ID ADQ18630 standard; DNA; 7433 BP.

XX

AC ADQ18630;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1449.

XX

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
ds.

XX

OS Homo sapiens.

XX

PN WO2004048938-A2.

Db	332		AAATCTCTGAACCTTTCACCTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	391
Qy	361		TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	420
Db	392		TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	451
Qy	421		GAAAAGTTGGACAAGCTGTTAAAATTACGTGAACCTCACTTATCATATAACAAAATCAGC	480
Db	452		GAAAAGTTGGACAAGCTGTTAAAATTACGTGAACCTCACTTATCATATAACAAAATCAGC	511
Qy	481		AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAGCTTAACCTTGCAGGAAATGAA	540
Db	512		AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAGCTTAACCTTGCAGGAAATGAA	571
Qy	541		ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	600
Db	572		ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	631
Qy	601		AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACCGCTTCAAGATTTG	660
Db	632		AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACCGCTTCAAGATTTG	691
Qy	661		ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC	720
Db	692		ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC	751
Qy	721		ATTTTCCACCTCCGTTTCATTGGAAAGTTTGGAAAGGTGAGCCAGTAACCACTCAGGATAGA	780
Db	752		ATTTTCCACCTCCGTTTCATTGGAAAGTTTGGAAAGGTGAGCCAGTAACCACTCAGGATAGA	811
Qy	781		CAGGAGGCTTTTGAGAGATTTCAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA	840
Db	812		CAGGAGGCTTTTGAGAGATTTCAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA	871
Qy	841		AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTCCCTTGAGGAAATT	900
Db	872		AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTCCCTTGAGGAAATT	931
Qy	901		AAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC	960
Db	932		AAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC	991
Qy	961		TGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA	1020
Db	992		TGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA	1051
Qy	1021		GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA	1080
Db	1052		GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA	1111
Qy	1081		ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA	1140
Db	1112		ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA	1171
Qy	1141		GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA	1200
Db	1172		GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA	1231
Qy	1201		GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1260

Db	1232	GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1291
Qy	1261	CAACTTAGAAATGATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAA	1320
Db	1292	CAACTTAGAAATGATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAA	1351
Qy	1321	GACAAAGAAAAAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATA	1380
Db	1352	GACAAAGAAAAAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATA	1411
Qy	1381	GAAAAGGCAGAACACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCT	1440
Db	1412	GAAAAGGCAGAACACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCT	1471
Qy	1441	ATACAACAAAAAGATTTTCAAGAGCAGGGAAGACCTTCTTTACAAGCAGTTGAGTGGT	1500
Db	1472	ATACAACAAAAAGATTTTCAAGAGCAGGGAAGACCTTCTTTACAAGCAGTTGAGTGGT	1531
Qy	1501	AGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAA	1560
Db	1532	AGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAA	1591
Qy	1561	AAGCAAAAGCAGGAAATTGCCGGAAAGCAGAAGGAGATTAAGGACCTGCAAAATAGCCATA	1620
Db	1592	AAGCAAAAGCAGGAAATTGCCGGAAAGCAGAAGGAGATTAAGGACCTGCAAAATAGCCATA	1651
Qy	1621	GATAGCCTGGATTCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAA	1680
Db	1652	GATAGCCTGGATTCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAA	1711
Qy	1681	GAACAACAGCTTGACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAG	1740
Db	1712	GAACAACAGCTTGACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAG	1771
Qy	1741	ATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACT	1800
Db	1772	ATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACT	1831
Qy	1801	GAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGG	1860
Db	1832	GAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGG	1891
Qy	1861	TTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGG	1920
Db	1892	TTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGG	1951
Qy	1921	AAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	1980
Db	1952	AAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	2011
Qy	1981	GACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGACAGAGCTA	2040
Db	2012	GACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGACAGAGCTA	2071
Qy	2041	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2100
Db	2072	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2131
Qy	2101	CTCAGTGCCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2160
Db	2132	CTCAGTGCCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2191

Qy	2161	CAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2220
Db	2192	CAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2251
Qy	2221	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAAAGCCAGTTC	2280
Db	2252	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAAAGCCAGTTC	2311
Qy	2281	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGAT	2340
Db	2312	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGAT	2371
Qy	2341	GACAATAATCTGTTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2400
Db	2372	GACAATAATCTGTTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2431
Qy	2401	GATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGT	2460
Db	2432	GATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGT	2491
Qy	2461	AAATTAGGAAC TGGGGAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2520
Db	2492	AAATTAGGAAC TGGGGAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2551
Qy	2521	GCTGATTTACAGAAACAATTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAA	2580
Db	2552	GCTGATTTACAGAAACAATTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAA	2611
Qy	2581	GCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCA	2640
Db	2612	GCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCA	2671
Qy	2641	ACTGGACAAGAAGAGTTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2700
Db	2672	ACTGGACAAGAAGAGTTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2731
Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCATATTGCAA	2760
Db	2732	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCATATTGCAA	2791
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAATTGAGGAAGCT	2820
Db	2792	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAATTGAGGAAGCT	2851
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Db	2852	GATGAAGAGAAGGAGAGAATTCTGGCCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2911
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
Db	2912	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2971
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Db	2972	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3031
Qy	3001	CTGAAGTCCCTTCATGGAAC TGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	3032	CTGAAGTCCCTTCATGGAAC TGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3091

Qy	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Db	3092	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3151
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Db	3152	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3211
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3240
Db	3212	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3271
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3300
Db	3272	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3331
Qy	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGA	3360
Db	3332	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGA	3391
Qy	3361	CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAAGACGA	3420
Db	3392	CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAAGACGA	3451
Qy	3421	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	3480
Db	3452	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	3511
Qy	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3540
Db	3512	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3571
Qy	3541	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600
Db	3572	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3631
Qy	3601	GTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3660
Db	3632	GTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3691
Qy	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCT	3720
Db	3692	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCT	3751
Qy	3721	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGCATG	3780
Db	3752	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGCATG	3811
Qy	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
Db	3812	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3871
Qy	3841	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC	3900
Db	3872	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC	3931
Qy	3901	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3960
Db	3932	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3991
Qy	3961	TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4020

Db	3992	 TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTATAAAATCAAAGAAGCGG	4051
Qy	4021	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4080
Db	4052	 GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4111
Qy	4081	CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4140
Db	4112	 CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4171
Qy	4141	CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4200
Db	4172	 CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4231
Qy	4201	CTTATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4260
Db	4232	 CTTATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4291
Qy	4261	ATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGA	4320
Db	4292	 ATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGA	4351
Qy	4321	CTCCTGGCAGAGGCTGAGAGTGAACCTTCATGCACTAAAGAAAAGACAAAAATGCTGTT	4380
Db	4352	 CTCCTGGCAGAGGCTGAGAGTGAACCTTCATGCACTAAAGAAAAGACAAAAATGCTGTT	4411
Qy	4381	GAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTA	4440
Db	4412	 GAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTA	4471
Qy	4441	GAAAGGAGAGCTCAGGAACTGCTGTAAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4500
Db	4472	 GAAAGGAGAGCTCAGGAACTGCTGTAAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4531
Qy	4501	CTCCAGGCTGATGCAAAGGATTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAA	4560
Db	4532	 CTCCAGGCTGATGCAAAGGATTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAA	4591
Qy	4561	GAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAG	4620
Db	4592	 GAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAG	4651
Qy	4621	GAAAAACTGACAGAAGAGCTTCAGAACTACAGAAAGACATAGAGATGGCAGAACGCAAT	4680
Db	4652	 GAAAAACTGACAGAAGAGCTTCAGAACTACAGAAAGACATAGAGATGGCAGAACGCAAT	4711
Qy	4681	GAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCC	4740
Db	4712	 GAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCC	4771
Qy	4741	GAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGAC	4800
Db	4772	 GAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGAC	4831
Qy	4801	AGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCA	4860
Db	4832	 AGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCA	4891
Qy	4861	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAAT	4920

Db	4892	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAAT	4951
Qy	4921	CACATTAGGGAAGTAAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	4980
Db	4952	CACATTAGGGAAGTAAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	5011
Qy	4981	G TTCAGATTAGTGAAAGAAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAG	5040
Db	5012	G TTCAGATTAGTGAAAGAAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAG	5071
Qy	5041	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5100
Db	5072	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5131
Qy	5101	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5160
Db	5132	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5191
Qy	5161	CAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTA	5220
Db	5192	CAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTA	5251
Qy	5221	GAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTC	5280
Db	5252	GAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTC	5311
Qy	5281	CTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCG	5340
Db	5312	CTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCG	5371
Qy	5341	TGTGTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAA	5400
Db	5372	TGTGTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAA	5431
Qy	5401	AAAAAGTTGGCACAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAG	5460
Db	5432	AAAAAGTTGGCACAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAG	5491
Qy	5461	CAATCAAACCTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAAGCTAGACCAA	5520
Db	5492	CAATCAAACCTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAAGCTAGACCAA	5551
Qy	5521	CTAAACAGAGACAAGTTGTCACTGCATAACGACATTTAGCAATGCAACAGCAGCTCCAA	5580
Db	5552	CTAAACAGAGACAAGTTGTCACTGCATAACGACATTTAGCAATGCAACAGCAGCTCCAA	5611
Qy	5581	GAAAAACGAGAAGCAGTAAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTG	5640
Db	5612	GAAAAACGAGAAGCAGTAAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTG	5671
Qy	5641	AACCTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAG	5700
Db	5672	AACCTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAG	5731
Qy	5701	CAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAA	5760
Db	5732	CAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAA	5791
Qy	5761	GAAGAGGAGACAAAACAACAACAACTTCAAGTGCTTCAGAATGAGATTGAAGAAAAACAAG	5820
Db	5792	GAAGAGGAGACAAAACAACAACAACTTCAAGTGCTTCAGAATGAGATTGAAGAAAAACAAG	5851

Qy	5821	CTCAAAC TAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAA	5880
Db	5852	CTCAAAC TAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAA	5911
Qy	5881	GAAAGCAAATTAGAAAC CAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAG	5940
Db	5912	GAAAGCAAATTAGAAAC CAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAG	5971
Qy	5941	GAATTAACAGACCAGAAAAAGCAAAC TGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAA	6000
Db	5972	GAATTAACAGACCAGAAAAAGCAAAC TGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAA	6031
Qy	6001	GAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTC	6060
Db	6032	GAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTC	6091
Qy	6061	TCCCAAAC TAAACGGCAGCTTT CAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAG	6120
Db	6092	TCCCAAAC TAAACGGCAGCTTT CAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAG	6151
Qy	6121	CTGTTGGCCCTCCAGAAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAAC	6180
Db	6152	CTGTTGGCCCTCCAGAAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAAC	6211
Qy	6181	CAGTTCTTGACAGAAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTT	6240
Db	6212	CAGTTCTTGACAGAAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTT	6271
Qy	6241	AAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGC	6300
Db	6272	AAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGC	6331
Qy	6301	ATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCATGAGCGGGCCAGG	6360
Db	6332	ATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCATGAGCGGGCCAGG	6391
Qy	6361	CGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATG	6420
Db	6392	CGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATG	6451
Qy	6421	GCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTT	6480
Db	6452	GCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTT	6511
Qy	6481	AAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6540
Db	6512	AAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6571
Qy	6541	GAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTG	6600
Db	6572	GAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTG	6631
Qy	6601	GAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTG	6660
Db	6632	GAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTG	6691
Qy	6661	AACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAA	6720
Db	6692	AACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAA	6751

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Qy      6721 CTGCGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCA 6780
        |||
Db      6752 CTGCGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCA 6811

Qy      6781 GAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAA 6840
        |||
Db      6812 GAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAA 6871

Qy      6841 GTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCGTCATCACCCAGT 6900
        |||
Db      6872 GTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCGTCATCACCCAGT 6931

Qy      6901 CTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAG 6960
        |||
Db      6932 CTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAG 6991

Qy      6961 AATGCCTCAGCCAGATGA 6978
        |||
Db      6992 AATGCCTCAGCCAGATGA 7009

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RESULT 3

ACC47248

ID ACC47248 standard; cDNA; 7222 BP.

XX

AC ACC47248;

XX

DT 11-AUG-2003 (first entry)

XX

DE Human SCAP encoding cDNA-Incyte Id. 2749809CB1.

XX

KW SCAP; structural and cytoskeleton-associated protein; nephrotropic;
 KW cytostatic; antiarteriosclerotic; hepatotropic; virucide; antibacterial;
 KW antihelminthic; cardiant; nootropic; neuroprotective; cerebroprotective;
 KW anticonvulsant; gene therapy; transgenic; human; gene; ss.

XX

OS Homo sapiens.

XX

PN WO2003008625-A2.

XX

PD 30-JAN-2003.

XX

PF 19-JUL-2002; 2002WO-US022866.

XX

PR 20-JUL-2001; 2001US-0306810P.

PR 27-JUL-2001; 2001US-0308338P.

PR 07-AUG-2001; 2001US-0310980P.

PR 17-AUG-2001; 2001US-0313098P.

PR 31-AUG-2001; 2001US-0316796P.

PR 07-SEP-2001; 2001US-0317899P.

PR 14-SEP-2001; 2001US-0322183P.

PR 28-SEP-2001; 2001US-0326101P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Jones KA, Swarnakar A, Gorvad AE, Hafalia AJA, Warren BA;
 PI Ison CH, Honchell CD, Nguyen DB, Barroso I, Das D, Lindquist EA;
 PI Lee EA, Yue H, Forsythe IJ, Ramkumar J, Griffin JA, Li JX, Yang J;
 PI Baughn MR, Borowsky ML, Thornton M, Yao MG, Walia NK, Burford N;
 PI Lal PG, Gururajan R, Lee S, Bulloch SA, Becha SD, Richardson TW;
 PI Elliott VS, Sprague WW, Tang YT, Azimzai Y, Lu Y, Zebarjadian Y;

XX
 DR WPI; 2003-239351/23.
 DR P-PSDB; ABR39818.
 XX
 PT New human structural and cytoskeleton-associated protein (SCAP), useful
 PT for diagnosing, treating and preventing diseases or conditions associated
 PT with aberrant SCAP expression, e.g. cancer, atherosclerosis or
 PT infections.
 XX
 PS Claim 5; Page 242-244; 267pp; English.
 XX
 CC The invention relates to novel human SCAP (structural and cytoskeleton-
 CC associated proteins and encoding polynucleotides. The SCAP polypeptides
 CC and polynucleotides are useful in diagnosing, treating and preventing
 CC diseases or conditions associated with aberrant expression of SCAP, such
 CC as cell motility disorders (e.g. ankylosing spondylitis), developmental
 CC disorders (e.g. renal tubular acidosis or dwarfism), cell proliferative
 CC disorders (e.g. cancer, arteriosclerosis, cirrhosis or hepatitis),
 CC infections (e.g. viral, bacterial or helminthic), heart and skeletal
 CC muscle disorders (e.g. muscular dystrophy or cardiomyopathy), and
 CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease,
 CC stroke, epilepsy or multiple sclerosis). These are also useful in
 CC assessing the effects of exogenous compounds on the expression of nucleic
 CC acid and amino acid sequences of SCAP. The SCAP or its fragments are
 CC useful in screening compounds for identifying modulators. The microarray
 CC is useful in monitoring or measuring protein-protein interactions, drug-
 CC target interactions, and gene expression profiles. Sequences ACC47235-271
 CC represent human SCAP polypeptides encoding cDNA sequences
 XX
 SQ Sequence 7222 BP; 2599 A; 1387 C; 1709 G; 1527 T; 0 U; 0 Other;

Query Match 95.7%; Score 6681.2; DB 8; Length 7222;
 Best Local Similarity 97.9%; Pred. No. 0;
 Matches 6834; Conservative 0; Mismatches 3; Indels 141; Gaps 1;

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Qy      1 ATGAAGAAAGGTTCTCAACAAAAAATATTCTCAAAGCAAAGATACCATCATCATCTCAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      137 ATGAAGAAAGGTTCTCAACAAAAAATATTCTCAAAGCAAAGATACCATCATCATCTCAC 196

Qy      61 TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTCACCTTTGATTGGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      197 TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTCACCTTTGATTGGA 256

Qy      121 TCAGAGACTCTACCTTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      257 TCAGAGACTCTACCTTTTTCATTCTGGAGGACAGTGGTGTGAGCAAAGTTGAGATTGCAGAT 316

Qy      181 GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      317 GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT 376

Qy      241 AGATATATTACAGAGGCCCTCATTAATAAACTTACTAAACAGGATAATTTGGCTTTGATA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      377 AGATATATTACAGAGGCCCTCATTAATAAACTTACTAAACAGGATAATTTGGCTTTGATA 436

Qy      301 AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      437 AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT 496

Qy      361 TTGGAATAATGTGTTAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db	497	TTGAAAAATGTGTTAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	556
Qy	421	GAAAAGTTGGACAAGCTGTTAAAAATTACGTGAAGTCAACTTATCATATAACAAAATCAGC	480
Db	557	GAAAAGTTGGACAAGCTGTTAAAAATTACGTGAAGTCAACTTATCATATAACAAAATCAGC	616
Qy	481	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	540
Db	617	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	676
Qy	541	ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	600
Db	677	ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	736
Qy	601	AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACCGCTTCAAGATTTG	660
Db	737	AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACTGCTTCAAGATTTG	796
Qy	661	ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC	720
Db	797	ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC	856
Qy	721	ATTTTCCACCTCCGTTTCATTGGAAAGTTTGGAAGGTGAGCCAGTAACCACTCAGGATAGA	780
Db	857	ATTTTCCACCTCCGTTTCATTGGAAAGTTTGGAAGGTGAGCCAGTAACCACTCAGGATAGA	916
Qy	781	CAGGAGGCTTTTGAGAGATTCAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA	840
Db	917	CAGGAGGCTTTTGAGAGATTCAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA	976
Qy	841	AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTTCCTTGAGGAAATT	900
Db	977	AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTTCCTTGAGGAAATT	1036
Qy	901	AAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC	960
Db	1037	AAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC	1096
Qy	961	TGTGAGGAACCTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA	1020
Db	1097	TGTGAGGAACCTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA	1156
Qy	1021	GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA	1080
Db	1157	GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA	1216
Qy	1081	ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA	1140
Db	1217	ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA	1276
Qy	1141	GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA	1200
Db	1277	GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA	1336
Qy	1201	GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1260
Db	1337	GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1396
Qy	1261	CAACTTAGAAATGATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAA	1320
Db	1397	CAACTTAGAAATGATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAA	1456

Qy	1321	GACAAAGAAAAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATA	1380
Db	1457	GACAAAGAAAAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATA	1516
Qy	1381	GAAAAGGCAGAACAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCT	1440
Db	1517	GAAAAGGCAGAACAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCT	1576
Qy	1441	ATACAACATAAAAAAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGTT	1500
Db	1577	ATACAACATAAAAAAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGTT	1636
Qy	1501	AGACTACAACCTGTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAA	1560
Db	1637	AGACTACAACCTGTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAA	1696
Qy	1561	AAGCAAAAGCAGGAAATTGCCGGAAAGCAGAAGGAGATTAAGGACCTGCAATAGCCATA	1620
Db	1697	AAGCAAAAGCAGGAAATTGCCGGAAAGCAGAAGGAGATTAAGGACCTGCAATAGCCATA	1756
Qy	1621	GATAGCCTGGATTCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAAGAGCGGTAAA	1680
Db	1757	GATAGCCTGGATTCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAAGAGCGGTAAA	1816
Qy	1681	GAACAACAGCTTGACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGATGAG	1740
Db	1817	GAACAACAGCTTGACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGATGAG	1876
Qy	1741	ATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACT	1800
Db	1877	ATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACT	1936
Qy	1801	GAAGGCCAGATAGCAGCAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGCG	1860
Db	1937	GAAGGCCAGATAGCAGCAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGCG	1996
Qy	1861	TTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGG	1920
Db	1997	TTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGG	2056
Qy	1921	AAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	1980
Db	2057	AAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	2116
Qy	1981	GACCAGCTGGAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGACAGAGCTA	2040
Db	2117	GACCAGCTGGAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGACAGAGCTA	2176
Qy	2041	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2100
Db	2177	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2236
Qy	2101	CTCAGTGCCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2160
Db	2237	CTCAGTGCCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2296
Qy	2161	CAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2220
Db	2297	CAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2356

Qy	2221	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCAGTTC	2280
Db	2357	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCAGTTC	2416
Qy	2281	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGAT	2340
Db	2417	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGAT	2476
Qy	2341	GACAATAATCTGTTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2400
Db	2477	GACAATAATCTGTTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2536
Qy	2401	GATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTTC	2460
Db	2537	GATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTTC	2596
Qy	2461	AAATTAGGAAGTGGGAAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2520
Db	2597	AAATTAGGAAGTGGGAAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2656
Qy	2521	GCTGATTTACAGAAACAATTCAAGTGAATTCCTTGACGCTCCAAGTGGGAAAGAGATGAA	2580
Db	2657	GCTGATTTACAGAAACAATTCAAGTGAATTCCTTGACGCTCCAAGTGGGAAAGAGATGAA	2716
Qy	2581	GCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCA	2640
Db	2717	GCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCA	2776
Qy	2641	ACTGGACAAGAAGAGTTCAAGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2700
Db	2777	ACTGGACAAGAAGAGTTCAAGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2836
Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCATATTTGCAA	2760
Db	2837	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCATATTTGCAA	2896
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCT	2820
Db	2897	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCT	2956
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Db	2957	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	3016
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
Db	3017	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	3076
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Db	3077	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3136
Qy	3001	CTGAAGTCCCTTCATGGAACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	3137	CTGAAGTCCCTTCATGGAACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3196
Qy	3061	GAAGCAGAGAGGTTTACAGCAGAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Db	3197	GAAGCAGAGAGGTTTACAGCAGAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAA	3256
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGAGCAGTTTCGACTTGAG	3180

Db	3257	 GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGAGCAGTTTCGACTTGAG	3316
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAAACTG	3240
Db	3317	 ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAAACTG	3376
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3300
Db	3377	 AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3436
Qy	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3360
Db	3437	 ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3496
Qy	3361	CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGA	3420
Db	3497	 CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGA	3556
Qy	3421	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	3480
Db	3557	 GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	3616
Qy	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTGTAGAAAACCA	3540
Db	3617	 GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTGTAGAAAACCA	3676
Qy	3541	CGCCCTGGGCAGCAGGATGCGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600
Db	3677	 CGCCCTGGGCAGCAGGATGCGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3736
Qy	3601	GTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3660
Db	3737	 GTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3796
Qy	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTGTGCCT	3720
Db	3797	 GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTGTGCCT	3856
Qy	3721	CCTCCTGGATACATGATGTATACTGTGCTTCTGTATGGTTCTCCTGTACCCAGGGCATG	3780
Db	3857	 CCTCCTGGATACATGATGTATACTGTGCTTCTGTATGGTTCTCCTGTACCCAGGGCATG	3916
Qy	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
Db	3917	 GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3976
Qy	3841	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC	3900
Db	3977	 GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC	4036
Qy	3901	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3960
Db	4037	 TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	4096
Qy	3961	TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4020
Db	4097	 TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4156
Qy	4021	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4080

Db	4157	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4216
Qy	4081	CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4140
Db	4217	CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4276
Qy	4141	CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4200
Db	4277	CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4336
Qy	4201	CTTATGACTGAACTAGAAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4260
Db	4337	CTTATGACTGAACTAGAAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4396
Qy	4261	ATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGA	4320
Db	4397	ATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGA	4456
Qy	4321	CTCCTGGCAGAGGCTGAGAGTGAACCTTTCATGCACTAAAGAAAAGACAAAAAATGCTGTT	4380
Db	4457	CTCCTGGCAGAGGCTGAGAGTGAACCTTTCATGCACTAAAGAAAAGACAAAAAATGCTGTT	4516
Qy	4381	GAAAAGTTCAGTGATGCCAAGAGAAGTTTATTGCAAACTGAGTCAGATGCTGAGGAATTA	4440
Db	4517	GAAAAGTTCAGTGATGCCAAGAGAAGTTTATTGCAAACTGAGTCAGATGCTGAGGAATTA	4576
Qy	4441	GAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4500
Db	4577	GAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4636
Qy	4501	CTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAA	4560
Db	4637	CTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAA	4696
Qy	4561	GAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAG	4620
Db	4697	GAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAG	4756
Qy	4621	GAAAAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAAT	4680
Db	4757	GAAAAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAAT	4816
Qy	4681	GAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCC	4740
Db	4817	GAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCC	4876
Qy	4741	GAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGAC	4800
Db	4877	GAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGAC	4936
Qy	4801	AGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCA	4860
Db	4937	AGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCA	4996
Qy	4861	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAAT	4920
Db	4997	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAAT	5056
Qy	4921	CACATTAGGGAAGTAAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	4980
Db	5057	CACATTAGGGAAGTAAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	5116

Qy	4981	G TTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAG	5040
Db	5117	G TTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAG	5176
Qy	5041	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5100
Db	5177	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5236
Qy	5101	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5160
Db	5237	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5296
Qy	5161	CAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTA	5220
Db	5297	CAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTA	5356
Qy	5221	GAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTC	5280
Db	5357	GAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTC	5416
Qy	5281	CTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCG	5340
Db	5417	CTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCG	5476
Qy	5341	TGTGTTGAGTGTGTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTG	5400
Db	5477	TGTGTTGAGTGTGTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTG	5536
Qy	5401	AAAAAGTTGGCACAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAG	5460
Db	5537	AAAAAGTTGGCACAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAG	5596
Qy	5461	CAATCAAACCTTAGAAAAGTTGGAATTGAATGTGAGAAAAGTGCAGCAGGAAGTACCA	5520
Db	5597	CAATCAAACCTTAGAAAAGTTGGAATTGAATGTGAGAAAAGTGCAGCAGGAAGTACCA	5656
Qy	5521	CTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAAGCAATGCAACAGCAGTCCAA	5580
Db	5657	CTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAAGCAATGCAACAGCAGTCCAA	5716
Qy	5581	GAAAAACGAGAAGCAGTAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTTG	5640
Db	5717	GAAAAACGAGAAGCAGTAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTTG	5776
Qy	5641	AACCTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAG	5700
Db	5777	AACCTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAG	5836
Qy	5701	CAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAA	5760
Db	5837	CAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAA	5896
Qy	5761	GAAGAGGAGACAAAACAACAACAACTTCAAGTGCTTCAGAATGAGATTGAAGAAAACAAG	5820
Db	5897	GAAGAGGAGACAAAACAACAACAACTTCAAGTGCTTCAGAATGAGATTGAAGAAAACAAG	5956
Qy	5821	CTCAAACCTAGTCCAACAAGAAATGATGTTTTAGAGACTCCAGAAAGAGAGAGAAAGTGAA	5880
Db	5957	CTCAAACCTAGTCCAACAAGAAATGATGTTTTAGAGACTCCAGAAAGAGAGAGAAAGTGAA	6016

Qy	5881	GAAAGCAAATTAGAAACCAAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAG	5940
Db	6017	GAAAGCAAATTAGAAACCAAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAG	6076
Qy	5941	GAATTAACAGACCAGAAAAGCAAAGTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAA	6000
Db	6077	GAATTAACAGACCAGAAAAGCAAAGTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAA	6136
Qy	6001	GAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTC	6060
Db	6137	GAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTC	6196
Qy	6061	TCCCAAATAACGGCAGCTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAG	6120
Db	6197	TCCCAAATAACGGCAGCTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAG	6256
Qy	6121	CTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAAC	6180
Db	6257	CTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAAC	6316
Qy	6181	CAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTT	6240
Db	6317	CAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTT	6376
Qy	6241	AAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGC	6300
Db	6377	AAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTT-----	6412
Qy	6301	ATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCATGAGCGGGCCAGG	6360
Db	6413	-----	6412
Qy	6361	CGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATG	6420
Db	6413	-----ATG	6415
Qy	6421	GCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTT	6480
Db	6416	GCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTT	6475
Qy	6481	AAATCTGAGGTGAAGGATGAAATCAGAACCAAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6540
Db	6476	AAATCTGAGGTGAAGGATGAAATCAGAACCAAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6535
Qy	6541	GAATAACAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTG	6600
Db	6536	GAATAACAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTG	6595
Qy	6601	GAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTG	6660
Db	6596	GAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTG	6655
Qy	6661	AACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAA	6720
Db	6656	AACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAA	6715
Qy	6721	CTGCGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCA	6780
Db	6716	CTGCGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCA	6775
Qy	6781	GAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAA	6840

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      |||
Db      6776 GAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAA 6835
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Qy      6841 GTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTTCAGCGTCATCACCCAGT 6900
      |||
Db      6836 GTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTTCAGCGTCATCACCCAGT 6895
      |||
Qy      6901 CTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAG 6960
      |||
Db      6896 CTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAG 6955
      |||
Qy      6961 AATGCCTCAGCCAGATGA 6978
      |||
Db      6956 AATGCCTCAGCCAGATGA 6973

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RESULT 4

AAS59864

ID AAS59864 standard; cDNA; 8452 BP.

XX

AC AAS59864;

XX

DT 16-JAN-2002 (first entry)

XX

DE Human novel cytokine encoding cDNA 790CIP2B_6 #2.

XX

KW Human; ss; cytokine; cell proliferation; cell differentiation;

KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;

KW nervous system disease; neuropathy; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease; spinal cord disorder;

KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;

KW platelet disorder; thrombocytopaenia; stem cell disorder;

KW aplastic anaemia; tissue regeneration; wound healing; ulcer;

KW osteoporosis; osteoarthritis; bone degenerative disorder;

KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;

KW severe combined immunodeficiency; infection; autoimmune disorder;

KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;

KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;

KW inflammatory bowel disease; food supplement.

XX

OS Homo sapiens.

XX

PN WO200175093-A1.

XX

PD 11-OCT-2001.

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PF 30-MAR-2001; 2001WO-US010484.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PR 22-SEP-2000; 2000US-00668680.

PR 23-OCT-2000; 2000US-00695618.

PR 30-NOV-2000; 2000US-00728711.

PR 14-MAR-2001; 2001US-00808701.

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PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

PI Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;

PI Drmanac RT;

XX

DR WPI; 2001-626432/72.

DR P-PSDB; AAU68572.

XX

PT New polypeptides and nucleic acids, useful for diagnosis, treatment of
PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
PT degenerative disorders, cancer and promoting wound healing.

XX

PS Claim 1; Page 287-289; 336pp; English.

XX

CC The invention relates to isolated human polypeptides (which may be
CC cytokines) and the polynucleotides encoding them. The protein is useful
CC for identifying a compound which binds to it (e.g. modulators, agonists
CC and antagonists). The polynucleotides are useful as an array for mismatch
CC detection. The proteins and nucleic acids are useful as nutritional
CC sources or supplements. The protein exhibits activity relating
CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,
CC stem cell growth factor activity, immune stimulating or immune
CC suppressing and activin or inhibin related activities. The proteins (and
CC antibodies raised against them) and nucleic acids are therefore useful in
CC the diagnosis and treatment of diseases and disorders such as cancer,
CC central and peripheral nervous system diseases and neuropathies,
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,
CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, and in tissue repair, healing of burns, incisions, ulcers, for
CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or
CC periodontal disease, lung or liver fibrosis, reperfusion injury in
CC various tissues, various immune deficiencies and disorders including
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,
CC diabetes mellitus, myasthenia gravis), allergic reactions and conditions;
CC such as asthma or other respiratory problems, coagulation disorders,
CC haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory
CC bowel disease, viral infection and are useful in altering bodily
CC characteristics. The present sequence encodes a novel protein of the
CC invention

XX

SQ Sequence 8452 BP; 3015 A; 1642 C; 2061 G; 1734 T; 0 U; 0 Other;

Query Match 78.3%; Score 5466.8; DB 4; Length 8452;

Best Local Similarity 93.5%; Pred. No. 0;

Matches 5909; Conservative 0; Mismatches 67; Indels 342; Gaps 6;

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Qy      808 GAAGAGGTAGAAAGACTGGAAAAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTT 867
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Db      2198 GAAGAGGTAGAAAGACTGGAAAAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTT 2257.

Qy      868 AAGAGCAAACAAACAAGGTTCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCA 927
      |||
Db      2258 AAGAGCAAACAAACAAGGTTCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCA 2317

Qy      928 TTAAAAGAGGAGGCCATGTTACAGAAACAGAGCTGTGAGGAAGCTCAAGAGTGACTTAAAC 987
      |||
Db      2318 TTAAAAGAGGAGGCCATGTTACAGAAACAGAGCTGTGAGGAAGCTCAAGAGTGACTTAAAC 2377

Qy      988 ACAAAAAATGAATTGCTAAAAACAGAAGACCATAGAATTAACACGAGCATGTCAGAAGCAA 1047
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Db      2378 ACAAAAAATGAATT----- 2391

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Qy	1048	TATGAGCTGGAACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAAT	1107
Db	2392	-----	2391
Qy	1108	TATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGC	1167
Db	2392	-----GTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGC	2437
Qy	1168	AAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAG	1227
Db	2438	AAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAG	2497
Qy	1228	GCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACCTTAGAAATGATCACATGAACTTG	1287
Db	2498	GCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACCTTAGAAATGATCACATGAACTTG	2557
Qy	1288	AGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCA	1347
Db	2558	AGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCA	2617
Qy	1348	CAAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAACAAATTTTGAGA	1407
Db	2618	CAAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAACAAATTTTGAGA	2677
Qy	1408	GCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACCTAAAAAAG-----	1455
Db	2678	GCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACCTAAAAAAGGAGGCTGTTGTT	2737
Qy	1456	-----	1455
Db	2738	CAGTACAGGCAAGAGATGATACTAGCACCAACCAGGAAGGTGCTGGTGGATGTGGAGAGA	2797
Qy	1456	-----ATTTCAGAAGCAGGGAAAGACCTTCTTTACAAGC--	1489
Db	2798	AAGCCAGCTGATTCCAGGAAACACTGGACAGTAGAACTGACAGGACTTAATGATGGGTTG	2857
Qy	1490	-----AGTTGAGTGGTAGACTACAACCTTGTAATAAAATTACGCCAGGAAGCT	1536
Db	2858	AAAGTAGGAGATGAGTTGAGTGGTAGACTACAACCTTGTAATAAAATTACGCCAGGAAGCT	2917
Qy	1537	CTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGAAAGCAGAAGGAG	1596
Db	2918	CTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGAAAGCAGAAGGAG	2977
Qy	1597	ATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCAT	1656
Db	2978	ATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCAT	3037
Qy	1657	ATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAA	1716
Db	3038	ATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAA	3097
Qy	1717	CAACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATT	1776
Db	3098	CAACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATT	3157
Qy	1777	AAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAG	1836
Db	3158	AAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAG	3217
Qy	1837	GATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCA	1896

Db	3218		GATTTAGAAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCA	3277
Qy	1897		ACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGA	1956
Db	3278		ACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGA	3337
Qy	1957		TTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAAT	2016
Db	3338		TTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAAT	3397
Qy	2017		ATGAGGAAGGAGCTTGCAGAGCTAGAAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCA	2076
Db	3398		ATGAGGAAGGAGCTTGCAGAGCTAGAAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCA	3457
Qy	2077		TCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTA	2136
Db	3458		TCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTA	3517
Qy	2137		AACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTT	2196
Db	3518		AACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTT	3577
Qy	2197		ACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAG	2256
Db	3578		ACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAG	3637
Qy	2257		AATGCCCTTGAAAAAGCCAGTTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCAT	2316
Db	3638		AATGCCCTTGAAAAAGCCAGTTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCAT	3697
Qy	2317		GCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAACAGCAACTTAAAGATTTC	2376
Db	3698		GCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAACAGCAACTTAAAGATTTC	3757
Qy	2377		CAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGT	2436
Db	3758		CAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGT	3817
Qy	2437		GTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCT	2496
Db	3818		GTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCT	3877
Qy	2497		TCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAAGTGAATTCCTTGCA	2556
Db	3878		TCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAAGTGAATTCCTTGCA	3937
Qy	2557		CGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATG	2616
Db	3938		CGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATG	3997
Qy	2617		GCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGA	2676
Db	3998		GCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGA	4057
Qy	2677		GCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATG	2736
Db	4058		GCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATG	4117
Qy	2737		GAGAATGAAATTCACTATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTT	2796

Db	4118	GAGAATGAAATTCACATATTTGCAAGAAAAATCTAAAAAAGTATGGAGGAAATCCAAGGCCTT	4177
Qy	2797	ACAGATCTCCAACCTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCCAATCCGA	2856
Db	4178	ACAGATCTCCAACCTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCCAATCCGA	4237
Qy	2857	GAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTA	2916
Db	4238	GAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTA	4297
Qy	2917	GATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCT	2976
Db	4298	GATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCT	4357
Qy	2977	GAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTTATGAAAATTAAC	3036
Db	4358	GAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTTATGAAAATTAAC	4417
Qy	3037	CAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCA	3096
Db	4418	CAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCA	4477
Qy	3097	GCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAG	3156
Db	4478	GCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAG	4537
Qy	3157	AAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAAACAGGTGTAGGTACTGGAGCAAACCTCA	3216
Db	4538	AAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAAACAGGTGTAGGTACTGGAGCAAACCTCA	4597
Qy	3217	CAGGTCCTAGAAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCA	3276
Db	4598	CAGGTCCTAGAAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCA	4657
Qy	3277	AGGCTGCAGAAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTT	3336
Db	4658	AGGCTGCAGAAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTT	4717
Qy	3337	TTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGC	3396
Db	4718	TTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGC	4777
Qy	3397	ATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCA	3456
Db	4778	ATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCA	4837
Qy	3457	AAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTTGGCCTTAAGTACTCA	3516
Db	4838	AAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTTGGCCTTAAGTACTCA	4897
Qy	3517	GCCTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAA	3576
Db	4898	GCCTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAA	4957
Qy	3577	CCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTG	3636
Db	4958	CCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTG	5017
Qy	3637	TTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGAC	3696
Db	5018	TTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGAC	5077

Qy	3697	CAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGAT	3756
Db	5078	CAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGAT	5137
Qy	3757	GGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAAT	3816
Db	5138	GGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAAT	5197
Qy	3817	AGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCCACCTCCTGCTGGGGCCCCCATG	3876
Db	5198	AGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCCACCTCCTGCTGGGGCCCCCATG	5257
Qy	3877	GTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCAT	3936
Db	5258	GTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCAT	5317
Qy	3937	TGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATG	3996
Db	5318	TGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATG	5377
Qy	3997	CAGCATTTAAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCG	4056
Db	5378	CAGCATTTAAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCG	5437
Qy	4057	GAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGC	4116
Db	5438	GAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGC	5497
Qy	4117	TTAGAGTGTGAAGTAGAAGAATTACATAGAACTGTCCAGAAACGTCAACAGCAAAAGGAC	4176
Db	5498	TTAGAGTGTGAAGTAGAAGAATTACATAGAACTGTCCAGAAACGTCAACAGCAAAAGGAC	5557
Qy	4177	TTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAA	4236
Db	5558	TTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAA	5617
Qy	4237	CATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGC	4296
Db	5618	CATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGC	5677
Qy	4297	TCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTTCATGCACT	4356
Db	5678	TCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTTCATGCACT	5737
Qy	4357	AAAGAAAA-----GACAAAAAATGCT	4377
Db	5738	AAAGAAAAGGTTTGTCTTCTTGTGGTTTGGGGTGTGAGCTCAGTGTGGACAAAAAATGCT	5797
Qy	4378	GTTGAAAAGTTCACCTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAA	4437
Db	5798	GTTGAAAAGTTCACCTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAA	5857
Qy	4438	TTAGAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGA	4497
Db	5858	TTAGAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGA	5917
Qy	4498	TCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTG	4557
Db	5918	TCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTG	5977

Qy	4558	AAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAAGCAAGAAG	4617
Db	5978	AAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAAGCAAGAAG	6037
Qy	4618	AAGGAAAAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGC	4677
Db	6038	AAGGAAAAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGC	6097
Qy	4678	AATGAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGA	4737
Db	6098	AATGAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGA	6157
Qy	4738	GCCGAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTG	4797
Db	6158	GCCGAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTG	6217
Qy	4798	GACAGGCAGTTAGGGCATAAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAG	4857
Db	6218	GACAGGCAGTTAGGGCATAAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAG	6277
Qy	4858	GCAAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGC	4917
Db	6278	GCAAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGC	6337
Qy	4918	AATCACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTA	4977
Db	6338	AATCACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTA	6397
Qy	4978	AATGTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAA	5037
Db	6398	AATGTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAA	6457
Qy	5038	GAGGAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAG	5097
Db	6458	GAGGAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAG	6517
Qy	5098	AATATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACAT	5157
Db	6518	AATATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACAT	6577
Qy	5158	GACCAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAAAAGTGGAG	5217
Db	6578	GACCAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAAAAGTGGAG	6637
Qy	5218	TTAGAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAG	5277
Db	6638	TTAGAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAG	6697
Qy	5278	CTCCTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAA	5337
Db	6698	CTCCTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAA	6757
Qy	5338	TCGTGTGTTGAGTGTTTGTAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGG	5397
Db	6758	TCGTGTGTTGAGTGTTTGTAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGG	6817
Qy	5398	GAAAAAAAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATG	5457
Db	6818	GAAAAAAAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATG	6877
Qy	5458	GAGCAATCAAACCTAGAAAAGTTGGAATTGAATGTCAGAAAAGTGCAGCAGGAAGTAGAC	5517

Db	6878	 GAGCAATCAAACCTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAACCTAGAC	6937
Qy	5518	CAACTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTC	5577
Db	6938	CAACTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTC	6997
Qy	5578	CAAGAAAAACGAGAAGCAGTAACTCACTG-----CAGGAGGAACTAGCTAATGTC	5628
Db	6998	CAAGACTTAGTAGATACTGGATTGGCACTGACCACCTCTAGTAAAGATGGCTTTATTAGT	7057
Qy	5629	CAAGACCATTGTAACCTAGCAAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTG	5688
Db	7058	AGTTTCCACTTGTCTTTACCTAAAGGACCTGCTTCACACCACCAAGCATCAGGATGTG	7117
Qy	5689	TTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAA	5748
Db	7118	TTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAA	7177
Qy	5749	GACTGTCAGAAAGAAGAGGAGACAAAACAACAACACTTCAAGTGCTTCAGAATGAGATT	5808
Db	7178	GACTGTCAGAAAGAAGAGGAGACAAAACAACAACACTTCAAGTGCTTCAGAATGAGATT	7237
Qy	5809	GAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAG	5868
Db	7238	GAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAG	7297
Qy	5869	AGAGAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCAC	5928
Db	7298	AGAGAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCAC	7357
Qy	5929	CAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTG	5988
Db	7358	CAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTG	7417
Qy	5989	CTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTG	6048
Db	7418	CTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTG	7477
Qy	6049	GAGAAGACACTCTCCCAAACCTAAACGGCAGCTTTTCAGAAAGGGAGCAGCAATTGGTGGAG	6108
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Qy	6109	AAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGC	6168
Db	7538	AAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGC	7597
Qy	6169	CTTCTGCGGAACCAAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTG	6228
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Db	7658	AAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAAACAG	7717
Qy	6289	GAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCAT	6348
Db	7718	GAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCAT	7777
Qy	6349	GAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTC	6408

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Db      7778 GAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTC 7837
Qy      6409 AAGAAACAGATGGCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCA 6468
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Db      7838 AAGAAACAGATGGCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCA 7897
Qy      6469 ATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAAT 6528
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Db      7898 ATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAAT 7957
Qy      6529 CAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTA 6588
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Db      7958 CAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTA 8017
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Db      8018 GAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTT 8077
Qy      6649 GAAGAAAACTGAACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCA 6708
        |||
Db      8078 GAAGAAAACTGAACTTTTCCCAAGTTCACATAAT----- 8112
Qy      6709 CTCCGGGAGAACTGCGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATG 6768
        |||
Db      8113 -----GGCCCAACTCCGACACTGTATG 8134
Qy      6769 TCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGT 6828
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Qy      6829 TTGAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCG 6888
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Qy      6889 TCATACCCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAA 6948
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Db      8315 AATCAGGCAGACAGTGTC 8332

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RESULT 5

AED08238

ID AED08238 standard; cDNA; 8452 BP.

XX

AC AED08238;

XX

DT 17-NOV-2005 (first entry)

XX

DE Human CP140 partial cDNA contig sequence.

XX

KW Immune stimulation; gene therapy; drug screening; transgenic animal;

KW food; inflammation; antiinflammatory; autoimmune disease;

KW immunosuppressive; immune disorder; autonomic nervous system disease;

KW cns-gen.; neurological disease; central nervous system disease; leukemia;

KW cytostatic; hematological disease; neoplasm; gene; ss; CP140 protein.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT CDS 2. .8452
 FT /*tag= a
 FT /product= "Human CP140 contig protein"
 FT /note= "No start codon"
 FT /partial
 XX
 PN US2005202422-A1.
 XX
 PD 15-SEP-2005.
 XX
 PF 08-NOV-2002; 2002US-00291128.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 30-MAR-2001; 2001WO-US010484.
 XX
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (CHEN/) CHEN R.
 PA (RENF/) REN F.
 PA (WANG/) WANG D.
 PA (WANG/) WANG J.
 PA (XUCC/) XU C.
 PA (XUEA/) XUE A J.
 PA (YANG/) YANG Y.
 PA (ZHAN/) ZHANG J.
 PA (ZHAO/) ZHAO Q A.
 PA (ZHOU/) ZHOU P.
 PA (GOOD/) GOODRICH R W.
 PA (DRMA/) DRMANAC R T.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ren F, Wang D, Wang J, Xu C;
 PI Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich RW, Drmanac RT;
 XX
 DR WPI; 2005-618089/63.
 DR P-PSDB; AED08281.
 XX
 PT New isolated polynucleotides, useful for treating, preventing, or
 PT ameliorating, e.g. Alzheimer's disease, Parkinson's disease, Huntington's
 PT disease, amyotrophic lateral sclerosis, or leukemia.
 XX
 PS Claim 1; SEQ ID NO 102; 60pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides capable of
 CC inducing an immune response. The polynucleotides and proteins are useful
 CC for treating, preventing or ameliorating a medical condition, e.g.
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, Shy-Drager syndrome or stroke. The
 CC proteins can be used for treating leukemia, inflammatory disorders and
 CC autoimmune disorders, e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes, myasthenia gravis or autoimmune inflammatory eye disease. They
 CC can also be used as nutritional sources and supplements, e.g. as a carbon
 CC source, nitrogen source or carbohydrate source. The sequences of the
 CC invention are also useful in gene therapy, drug screening and in
 CC production of transgenic animals. The present sequence is the human CP140
 CC partial contig cDNA of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20050202422.
 XX

SQ Sequence 8452 BP; 3015 A; 1642 C; 2061 G; 1734 T; 0 U; 0 Other;

Query Match 78.3%; Score 5466.8; DB 14; Length 8452;
 Best Local Similarity 93.5%; Pred. No. 0;
 Matches 5909; Conservative 0; Mismatches 67; Indels 342; Gaps 6;

Qy	808	GAAGAGGTAGAAAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTT	867
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Qy	868	AAGAGCAAACAAACAAGGTTCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCA	927
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Qy	1048	TATGAGCTGGAACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAAT	1107
Db	2392	-----	2391
Qy	1108	TATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGC	1167
Db	2392	-----GTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGC	2437
Qy	1168	AAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAG	1227
Db	2438	AAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAG	2497
Qy	1228	GCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACCTTAGAAATGATCACATGAACTTG	1287
Db	2498	GCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACCTTAGAAATGATCACATGAACTTG	2557
Qy	1288	AGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCA	1347
Db	2558	AGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCA	2617
Qy	1348	CAAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAACACAAATTTTGAGA	1407
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Qy	1408	GCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACCTAAAAAAG-----	1455
Db	2678	GCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACCTAAAAAAGGAGGCTGTTGTT	2737
Qy	1456	-----	1455
Db	2738	CAGTACAGGCAAGAGATGATACTAGCACCAACCAGGAAGGTGCTGGTGGATGTGGAGAGA	2797
Qy	1456	-----ATTCAGAAGCAGGGAAGACCTTCTTTACAAGC--	1489
Db	2798	AAGCCAGCTGATTCCAGGAAACACTGGACAGTAGAACTGACAGGACTTAATGATGGGTTG	2857
Qy	1490	-----AGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCT	1536
Db	2858	AAAGTAGGAGATGAGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCT	2917

Qy	1537	CTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGAAAGCAGAAGGAG	1596
Db	2918	CTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGAAAGCAGAAGGAG	2977
Qy	1597	ATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCAT	1656
Db	2978	ATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCAT	3037
Qy	1657	ATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAA	1716
Db	3038	ATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAA	3097
Qy	1717	CAACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATT	1776
Db	3098	CAACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATT	3157
Qy	1777	AAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAG	1836
Db	3158	AAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAG	3217
Qy	1837	GATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCA	1896
Db	3218	GATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCA	3277
Qy	1897	ACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGA	1956
Db	3278	ACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGA	3337
Qy	1957	TTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAAT	2016
Db	3338	TTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAAT	3397
Qy	2017	ATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCA	2076
Db	3398	ATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCA	3457
Qy	2077	TCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTA	2136
Db	3458	TCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTA	3517
Qy	2137	AACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTT	2196
Db	3518	AACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTT	3577
Qy	2197	ACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAG	2256
Db	3578	ACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAG	3637
Qy	2257	AATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCAT	2316
Db	3638	AATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCAT	3697
Qy	2317	GCAAACTTAAACACTTGCAAGGATGACAATAATCTGTAAAACAGCAACTTAAAGATTTC	2376
Db	3698	GCAAACTTAAACACTTGCAAGGATGACAATAATCTGTAAAACAGCAACTTAAAGATTTC	3757
Qy	2377	CAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGT	2436
Db	3758	CAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGT	3817

Qy	2437	GTGGATGAGCTAAGAAGAAAAGTCTGCTGATTTACAGAAACAATTCAGTGAAATTCCTTGCA	2496
Db	3818	GTGGATGAGCTAAGAAGAAAAGTCTGCTGATTTACAGAAACAATTCAGTGAAATTCCTTGCA	3877
Qy	2497	TCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCCTTGCA	2556
Db	3878	TCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCCTTGCA	3937
Qy	2557	CGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATG	2616
Db	3938	CGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATG	3997
Qy	2617	GCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGA	2676
Db	3998	GCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGA	4057
Qy	2677	GCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATG	2736
Db	4058	GCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATG	4117
Qy	2737	GAGAATGAAATTCAGTATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTT	2796
Db	4118	GAGAATGAAATTCAGTATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTT	4177
Qy	2797	ACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCAGGCCTTCCGA	2856
Db	4178	ACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCAGGCCTTCCGA	4237
Qy	2857	GAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTA	2916
Db	4238	GAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTA	4297
Qy	2917	GATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCT	2976
Db	4298	GATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCT	4357
Qy	2977	GAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGAAAATTAAC	3036
Db	4358	GAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGAAAATTAAC	4417
Qy	3037	CAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCA	3096
Db	4418	CAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCA	4477
Qy	3097	GCCAGAGATCTCAGGAGCAGAAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAG	3156
Db	4478	GCCAGAGATCTCAGGAGCAGAAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAG	4537
Qy	3157	AAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAATCA	3216
Db	4538	AAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAATCA	4597
Qy	3217	CAGGTCTAGAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCA	3276
Db	4598	CAGGTCTAGAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCA	4657
Qy	3277	AGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTT	3336
Db	4658	AGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTT	4717
Qy	3337	TTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGC	3396

Db	4718	 TTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGC	4777
Qy	3397	ATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCA	3456
Db	4778	 ATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCA	4837
Qy	3457	AAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCA	3516
Db	4838	 AAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCA	4897
Qy	3517	GCCTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAA	3576
Db	4898	 GCCTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAA	4957
Qy	3577	CCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTACATAAACTG	3636
Db	4958	 CCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTACATAAACTG	5017
Qy	3637	TTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGAC	3696
Db	5018	 TTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGAC	5077
Qy	3697	CAAGAAGAACCCCCATTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGAT	3756
Db	5078	 CAAGAAGAACCCCCATTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGAT	5137
Qy	3757	GGTTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAAT	3816
Db	5138	 GGTTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAAT	5197
Qy	3817	AGCCGACCTCTACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATG	3876
Db	5198	 AGCCGACCTCTACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATG	5257
Qy	3877	GTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCAT	3936
Db	5258	 GTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCAT	5317
Qy	3937	TGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATG	3996
Db	5318	 TGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATG	5377
Qy	3997	CAGCATT'TAAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCG	4056
Db	5378	 CAGCATT'TAAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCG	5437
Qy	4057	GAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGC	4116
Db	5438	 GAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGC	5497
Qy	4117	TTAGAGTGTGAAGTAGAAGAATTACATAGAACTGTCCAGAAACGTCAACAGCAAAAGGAC	4176
Db	5498	 TTAGAGTGTGAAGTAGAAGAATTACATAGAACTGTCCAGAAACGTCAACAGCAAAAGGAC	5557
Qy	4177	TTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAA	4236
Db	5558	 TTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAA	5617
Qy	4237	CATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGC	4296

Db	5618	CATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGTGAAACGTCGC	5677
Qy	4297	TCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTTCATGCACT	4356
Db	5678	TCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTTCATGCACT	5737
Qy	4357	AAAGAAAA-----GACAAAAAATGCT	4377
Db	5738	AAAGAAAAGGTTTGTCTTCTTGTGGTTTGGGGTGTGAGCTCAGTGTGGACAAAAAATGCT	5797
Qy	4378	GTTGAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAAGTCTGAGTCAGATGCTGAGGAA	4437
Db	5798	GTTGAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAAGTCTGAGTCAGATGCTGAGGAA	5857
Qy	4438	TTAGAAAAGGAGAGCTCAGGAAAGTCTGTTAACTCGTCAAAGCTGATCAGCAGCTAAGA	4497
Db	5858	TTAGAAAAGGAGAGCTCAGGAAAGTCTGTTAACTCGTCAAAGCTGATCAGCAGCTAAGA	5917
Qy	4498	TCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTG	4557
Db	5918	TCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTG	5977
Qy	4558	AAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAG	4617
Db	5978	AAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAG	6037
Qy	4618	AAGGAAAAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGC	4677
Db	6038	AAGGAAAAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGC	6097
Qy	4678	AATGAGGATCACCACCTGCAGGTCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGA	4737
Db	6098	AATGAGGATCACCACCTGCAGGTCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGA	6157
Qy	4738	GCCGAGCTGGAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTG	4797
Db	6158	GCCGAGCTGGAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTG	6217
Qy	4798	GACAGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAG	4857
Db	6218	GACAGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAG	6277
Qy	4858	GCAAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGC	4917
Db	6278	GCAAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGC	6337
Qy	4918	AATCACATTAGGGAAGTAAATCTCTTCTGGAAGAACTGAGTTTTCAGAAAGGAGAACTA	4977
Db	6338	AATCACATTAGGGAAGTAAATCTCTTCTGGAAGAACTGAGTTTTCAGAAAGGAGAACTA	6397
Qy	4978	AATGTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAA	5037
Db	6398	AATGTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAA	6457
Qy	5038	GAGGAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAG	5097
Db	6458	GAGGAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAG	6517
Qy	5098	AATATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACAT	5157
Db	6518	AATATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACAT	6577

Qy	5158	GACCAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAG	5217
Db	6578	GACCAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAG	6637
Qy	5218	TTAGAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAG	5277
Db	6638	TTAGAGAATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAG	6697
Qy	5278	CTCCTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAA	5337
Db	6698	CTCCTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAA	6757
Qy	5338	TCGTGTGTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGG	5397
Db	6758	TCGTGTGTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGG	6817
Qy	5398	GAAAAAAAGTTGGCACAACCAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATG	5457
Db	6818	GAAAAAAAGTTGGCACAACCAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATG	6877
Qy	5458	GAGCAATCAAACCTTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAAC TAGAC	5517
Db	6878	GAGCAATCAAACCTTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAAC TAGAC	6937
Qy	5518	CAACTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTC	5577
Db	6938	CAACTAAACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTC	6997
Qy	5578	CAAGAAAAACGAGAAGCAGTAAACTCACTG-----CAGGAGGAACTAGCTAATGTC	5628
Db	6998	CAAGACTTAGTAGATACTGGATTGGCACTGACCACCTCTAGTAAAGATGGCTTTATTAGT	7057
Qy	5629	CAAGACCATTTGAACCTAGCAAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTG	5688
Db	7058	AGTTTCCACTTGTTCTTTTACCTAAAGGACCTGCTTCACACCACCAAGCATCAGGATGTG	7117
Qy	5689	TTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAA	5748
Db	7118	TTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAA	7177
Qy	5749	GACTGTCAGAAAGAAGAGGAGACAAAACAACAACACTTCAAGTGCTTCAGAATGAGATT	5808
Db	7178	GACTGTCAGAAAGAAGAGGAGACAAAACAACAACACTTCAAGTGCTTCAGAATGAGATT	7237
Qy	5809	GAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAAGAG	5868
Db	7238	GAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAAGAG	7297
Qy	5869	AGAGAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCAC	5928
Db	7298	AGAGAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCAC	7357
Qy	5929	CAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTG	5988
Db	7358	CAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTG	7417
Qy	5989	CTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTG	6048
Db	7418	CTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTG	7477

Qy	6049	GAGAAGACACTCTCCCAAACCTAAACGGCAGCTTTTCAGAAAGGGAGCAGCAATTGGTGGAG	6108
Db	7478	GAGAAGACACTCTCCCAAACCTAAACGGCAGCTTTTCAGAAAGGGAGCAGCAATTGGTGGAG	7537
Qy	6109	AAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGC	6168
Db	7538	AAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGC	7597
Qy	6169	CTTCTGCGGAACCAAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTG	6228
Db	7598	CTTCTGCGGAACCAAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTG	7657
Qy	6229	AAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAAACAG	6288
Db	7658	AAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAAACAG	7717
Qy	6289	GAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCAT	6348
Db	7718	GAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAACTGGTAGCCAGGACAACCAT	7777
Qy	6349	GAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTC	6408
Db	7778	GAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTC	7837
Qy	6409	AAGAAACAGATGGCAAACCAAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCA	6468
Db	7838	AAGAAACAGATGGCAAACCAAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCA	7897
Qy	6469	ATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAAT	6528
Db	7898	ATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAAT	7957
Qy	6529	CAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTA	6588
Db	7958	CAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTA	8017
Qy	6589	GAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTT	6648
Db	8018	GAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTT	8077
Qy	6649	GAAGAAAACTGAACTTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCA	6708
Db	8078	GAAGAAAACTGAACTTTTCCCAAGTTCACATAAT-----	8112
Qy	6709	CTCCGGGAGAACTGCGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATG	6768
Db	8113	-----GGCCCAACTCCGACACTGTATG	8134
Qy	6769	TCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGT	6828
Db	8135	TCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGT	8194
Qy	6829	TTGAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCG	6888
Db	8195	TTGAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCAGCACCTCTGCAGATTCAGCG	8254
Qy	6889	TCATCACCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAA	6948
Db	8255	TCATCACCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAA	8314
Qy	6949	AATCAGGAAAAGAAATGCC	6966

||||| | | | |
 Db 8315 AATCAGGCAGACAGTGTC 8332

RESULT 6

ADC30206

ID ADC30206 standard; cDNA; 6075 BP.

XX

AC ADC30206;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human novel cDNA sequence, SEQ ID NO:288.

XX

KW Human; diagnostic; drug screening; forensics; gene mapping;

KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;

KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;

KW ulcers; osteoporosis; autoimmune disease; cancer;

KW molecular weight marker; food supplement; antiparkinsonian; nootropic;

KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;

KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;

KW gene therapy; chromosome 9q34.11-34.13; gene; ss.

XX

OS Homo sapiens.

XX

PN WO2003029271-A2.

XX

PD 10-APR-2003.

XX

PF 24-SEP-2002; 2002WO-US030474.

XX

PR 24-SEP-2001; 2001US-0324631P.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;

PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;

PI Haley-Vicente D, Drmanac RT;

XX

DR WPI; 2003-371981/35.

DR P-PSDB; ADC31177.

XX

PT New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.

XX

PS Claim 1; SEQ ID NO 288; 1185pp; English.

XX

CC The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention; the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of
 CC identifying a compound which binds to a polypeptide of the invention. The
 CC invention further discloses methods of preventing, treating or
 CC ameliorating a medical condition; kits comprising polynucleotide probes
 CC and/or monoclonal antibodies for carrying out the methods of the

invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628-ADC33394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 6075 BP; 2119 A; 1177 C; 1516 G; 1263 T; 0 U; 0 Other;

Query Match 76.0%; Score 5302.8; DB 10; Length 6075;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 5313; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

[illegible]

Db	952	CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA	1011
Qy	2189	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	2248
Db	1012	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	1071
Qy	2249	CCCTCAAGAATGCCCTTGAAAAAGCCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG	2308
Db	1072	CCCTCAAGAATGCCCTTGAAAAAGCCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG	1131
Qy	2309	AGCTCCATGCAAACTTAAACACTTGAGGATGACAATAATCTGTTAAACAGCAACTTA	2368
Db	1132	AGCTCCATGCAAACTTAAACACTTGAGGATGACAATAATCTGTTAAACAGCAACTTA	1191
Qy	2369	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	2428
Db	1192	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	1251
Qy	2429	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCC	2488
Db	1252	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCC	1311
Qy	2489	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	2548
Db	1312	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	1371
Qy	2549	TTCTTGCACGCTCCAAGTGGGAAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAG	2608
Db	1372	TTCTTGCACGCTCCAAGTGGGAAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAG	1431
Qy	2609	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCT	2668
Db	1432	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCT	1491
Qy	2669	GTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCC	2728
Db	1492	GTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCC	1551
Qy	2729	AGCAAATGGAGAATGAAATTCATATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCC	2788
Db	1552	AGCAAATGGAGAATGAAATTCATATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCC	1611
Qy	2789	AAGGCCTTACAGATCTCAACTTCAGGAAGCTGATGAAGAGAAGGAGAGAAATCTGGCCC	2848
Db	1612	AAGGCCTTACAGATCTCAACTTCAGGAAGCTGATGAAGAGAAGGAGAGAAATCTGGCCC	1671
Qy	2849	AACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTT	2908
Db	1672	AACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTT	1731
Qy	2909	TTGGTTTGTAGATAAAGAACTGAAGAAAAGTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAG	2968
Db	1732	TTGGTTTGTAGATAAAGAACTGAAGAAAAGTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAG	1791
Qy	2969	CCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGA	3028
Db	1792	CCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGA	1851
Qy	3029	AAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTCAGCAGAAAGGCAG	3088
Db	1852	AAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTCAGCAGAAAGGCAG	1911

Qy	3089	CACAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCC	3148
Db	1912	CACAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCC	1971
Qy	3149	TCAGGCAGAAGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAG	3208
Db	1972	TCAGGCAGAAGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAG	2031
Qy	3209	CAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAG	3268
Db	2032	CAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAG	2091
Qy	3269	AGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTG	3328
Db	2092	AGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTG	2151
Qy	3329	AAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACA	3388
Db	2152	AAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACA	2211
Qy	3389	TAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCAC	3448
Db	2212	TAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCAC	2271
Qy	3449	CATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTA	3508
Db	2272	CATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTA	2331
Qy	3509	AGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAGCAGGATGGGAAGGAAG	3568
Db	2332	AGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAGCAGGATGGGAAGGAAG	2391
Qy	3569	GCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTAC	3628
Db	2392	GCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTAC	2451
Qy	3629	ATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGC	3688
Db	2452	ATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGC	2511
Qy	3689	TGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGC	3748
Db	2512	TGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGC	2571
Qy	3749	TTCTTGATGGTTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGC	3808
Db	2572	TTCTTGATGGTTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGC	2631
Qy	3809	CAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCCACCTCCTGCTGGGG	3868
Db	2632	CAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCCACCTCCTGCTGGGG	2691
Qy	3869	CCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTG	3928
Db	2692	CCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTG	2751
Qy	3929	TGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAG	3988
Db	2752	TGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAG	2811

Qy	3989	ACATAATGCAGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGC	4048
Db	2812	ACATAATGCAGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGC	2871
Qy	4049	GGCAGTCGGAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGA	4108
Db	2872	GGCAGTCGGAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGA	2931
Qy	4109	AGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACATAGAAGTGTCCAGAAACGTCAACAGC	4168
Db	2932	AGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACATAGAAGTGTCCAGAAACGTCAACAGC	2991
Qy	4169	AAAAGGACTTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAAT	4228
Db	2992	AAAAGGACTTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAAT	3051
Qy	4229	CACTCAAACATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGA	4288
Db	3052	CACTCAAACATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGA	3111
Qy	4289	AACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTT	4348
Db	3112	AACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTT	3171
Qy	4349	CATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCACTGATGCCAAGAGAAGTT	4408
Db	3172	CATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCACTGATGCCAAGAGAAGTT	3231
Qy	4409	TATTGCAAACCTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAACTGCTGTTA	4468
Db	3232	TATTGCAAACCTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAACTGCTGTTA	3291
Qy	4469	ACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGC	4528
Db	3292	ACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGC	3351
Qy	4529	AGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAG	4588
Db	3352	AGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAG	3411
Qy	4589	ACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAGCTTCAGAAAC	4648
Db	3412	ACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAGCTTCAGAAAC	3471
Qy	4649	TACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAGGTCCTTAAAG	4708
Db	3472	TACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAGGTCCTTAAAG	3531
Qy	4709	AATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGA	4768
Db	3532	AATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGA	3591
Qy	4769	CAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAAAAGGAGGAGC	4828
Db	3592	CAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAAAAGGAGGAGC	3651
Qy	4829	TGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAAGCTCTGAGAC	4888
Db	3652	TGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAAGCTCTGAGAC	3711
Qy	4889	TGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAATCTCTTCTGG	4948

Db	3712	 TGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAATCTCTCTGG	3771
Qy	4949	AAGAACTGAGTTTTTCAGAAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAAC	5008
Db	3772	 AAGAACTGAGTTTTTCAGAAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAAC	3831
Qy	5009	TTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTTGTTTTAAGGC	5068
Db	3832	 TTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTTGTTTTAAGGC	3891
Qy	5069	AGATGTCTAAACATAAAACCGAACTAAAGAATATTCTGGACATGTTGCAACTTGAAAACC	5128
Db	3892	 AGATGTCTAAACATAAAACCGAACTACAGAATATTCTGGACATGTTGCAACTTGAAAACC	3951
Qy	5129	ATGAGCTACAAGGTTTGAAGCTACAACATGACCAAAGGGTATCTGAATTAGAGAAGACTC	5188
Db	3952	 ATGAGCTACAAGGTTTGAAGCTACAACATGACCAAAGGGTATCTGAATTAGAGAAGACTC	4011
Qy	5189	AGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAGAATTTGCAGCAGATATCCCAGCAGC	5248
Db	4012	 AGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAGAATTTGCAGCAGATATCCCAGCAGC	4071
Qy	5249	AGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTTGAGAGGGATAAACGAGAAATAGAAC	5308
Db	4072	 AGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTTGAGAGGGATAAACGAGAAATAGAAC	4131
Qy	5309	GAATGACTGCTGAGTCCCGAGCTTTACAATCGTGTGTTGAGTGTTTGAGCAAAGAAAAGG	5368
Db	4132	 GAATGACTGCTGAGTCCCGAGCTTTACAATCGTGTGTTGAGTGTTTGAGCAAAGAAAAGG	4191
Qy	5369	AAGATCTCCAAGAGAAATGTGACATTTGGGAAAAAAGTTGGCACAACCAAAGGGTTT	5428
Db	4192	 AAGATCTCCAAGAGAAATGTGACATTTGGGAAAAAAGTTGGCACAACCAAAGGGTTT	4251
Qy	5429	TAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAATCAAACCTAGAAAAGTTGGAATTGA	5488
Db	4252	 TAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAATCAAACCTAGAAAAGTTGGAATTGA	4311
Qy	5489	ATGTCAGAAAACCTGCAGCAGGAACTAGACCAACTAAACAGAGACAAGTTGTCACTGCATA	5548
Db	4312	 ATGTCAGAAAACCTGCAGCAGGAACTAGACCAACTAAACAGAGACAAGTTGTCACTGCATA	4371
Qy	5549	ACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAAAAACGAGAAGCAGTAACTCACTGC	5608
Db	4372	 ACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAAAAACGAGAAGCAGTAACTCACTGC	4431
Qy	5609	AGGAGGAACTAGCTAATGTCCAAGACCATTGTAACCTAGCAAAACAGGACCTGCTTCACA	5668
Db	4432	 AGGAGGAACTAGCTAATGTCCAAGACCATTGTAACCTAGCAAAACAGGACCTGCTTCACA	4491
Qy	5669	CCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTG	5728
Db	4492	 CCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTG	4551
Qy	5729	AATGGGCAAATAGGTTTGAAGACTGTCAGAAAGAAGAGGAGACAAAACAACAACACTTC	5788
Db	4552	 AATGGGCAAATAGGTTTGAAGACTGTCAGAAAGAAGAGGAGACAAAACAACAACACTTC	4611
Qy	5789	AAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGT	5848

Db	4612	AAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGT	4671
Qy	5849	TTCAGAGACTCCAGAAAGAGAGAGAAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGA	5908
Db	4672	TTCAGAGACTCCAGAAAGAGAGAGAAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGA	4731
Qy	5909	CACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGG	5968
Db	4732	CACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGG	4791
Qy	5969	ACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGG	6028
Db	4792	ACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGG	4851
Qy	6029	AGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAAACCTAAACGGCAGCTTTCAGAAA	6088
Db	4852	AGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAAACCTAAACGGCAGCTTTCAGAAA	4911
Qy	6089	GGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATT	6148
Db	4912	GGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATT	4971
Qy	6149	CTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAAGTTCTTGACAGAAAGAAAGAAAGCTG	6208
Db	4972	CTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAAGTTCTTGACAGAAAGAAAGAAAGCTG	5031
Qy	6209	AGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAA	6268
Db	5032	AGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAA	5091
Qy	6269	ACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAAC	6328
Db	5092	ACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAAC	5151
Qy	6329	TGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGC	6388
Db	5152	TGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGC	5211
Qy	6389	AGTATGAGTACACGGAGCTCAAGAAACAGATGGCAAACCAAAAAGATTTGGAGAGAAGAC	6448
Db	5212	AGTATGAGTACACGGAGCTCAAGAAACAGATGGCAAACCAAAAAGATTTGGAGAGAAGAC	5271
Qy	6449	AAATGGAAATCAGTGATGCAATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAA	6508
Db	5272	AAATGGAAATCAGTGATGCAATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAA	5331
Qy	6509	CCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTT	6568
Db	5332	CCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTT	5391
Qy	6569	TGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTA	6628
Db	5392	TGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTA	5451
Qy	6629	CCATGAATGAGGGACCTTTTGAAGAAAACTGAACTTTTCCCAAGTTCACATAATGGATG	6688
Db	5452	CCATGAATGAGGGACCTTTTGAAGAAAACTGAACTTTTCCCAAGTTCACATAATGGATG	5511
Qy	6689	AACACTGGCGTGGAGAAGCACTCCGGGAGAACTGCGTCACCGGGAAGACCGACTCAAGG	6748
Db	5512	AACACTGGCGTGGAGAAGCACTCCGGGAGAACTGCGTCACCGGGAAGACCGACTCAAGG	5571

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Qy      6749 CCCAACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGA 6808
        |||
Db      5572 CCCAACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGA 5631

Qy      6809 CAGAGGGCACTTTACACAGTTTGAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCA 6868
        |||
Db      5632 CAGAGGGCACTTTACACAGTTTGAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCA 5691

Qy      6869 GCACCTCTGCAGATTTCAGCGTCATCACCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAG 6928
        |||
Db      5692 GCACCTCTGCAGATTTCAGCGTCATCACCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAG 5751

Qy      6929 AGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA 6978
        |||
Db      5752 AGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA 5801

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RESULT 7

ADQ23084

ID ADQ23084 standard; DNA; 6244 BP.

XX

AC ADQ23084;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5904.

XX

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.

XX

OS Homo sapiens.

XX

PN WO2004048938-A2.

XX

PD 10-JUN-2004.

XX

PF 26-NOV-2003; 2003WO-US038193.

XX

PR 26-NOV-2002; 2002US-0429739P.

XX

PA (PROT-) PROTEIN DESIGN LABS INC.

XX

PI Aziz N, Ginsburg WM, Zlotnik A;

XX

DR WPI; 2004-441208/41.

XX

PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX

PS Example 2; SEQ ID NO 5904; 210pp; English.

XX

CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has

CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX
SQ Sequence 6244 BP; 2271 A; 1206 C; 1524 G; 1193 T; 0 U; 50 Other;

Query Match 76.0%; Score 5300.8; DB 12; Length 6244;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 5330; Conservative 0; Mismatches 52; Indels 18; Gaps 1;

Qy 1579 GCCGGAAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAA 1638

Db 1 GCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAA 60

Qy 1639 GACCCAAAAACATTCCCATATGAAGGCTCAAAAAGAGCGGTAAAGAACAACAGCTTGACATT 1698

Db 61 GACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATT 120

Qy 1699 ATGAACAAAGCAGTACCAACAACCTTGAAAGTCGTTGGATGAGATACTTTCTAGAATTGCT 1758

Db 121 ATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCT 180

Qy 1759 AAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCA 1818

Db 181 AAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCA 240

Qy 1819 AATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTCGAAGAATACCTGGGG 1878

Db 241 AATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATACCTGGGG 300

QY 1879 ACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAA 1938

Db 301 ACCATTAAAGGCCAGGCAACTCAGGCCAGAAATGAGTGCAGGAAGCTGCGGGATGAGAAA 360

Qy 1939 GAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTT 1998

Db 361 GAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTT 420

Qy 1999 GCCATGGATGCAGAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAG 2058
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 421 GCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAG 480

Qy 2059 CAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCT 2118

Db 481 CAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCT 540

Qy 2119 GAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTG 2178
 |||||

Db 541 GAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTG 600

Qy 2179 GAAAAAGTAACAAGACTTACCCAGTTAGAACAAATCAGCCCTTCAAGCAGAACTTGAGAAG 2238

Db 601 GAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAG 660

Qy 2239 GAAAGGCAAGCCCTCAAGAATGCCCTTGGAAAAGCCCAGTTCTCAGAAGAAAAAGGAGCAA 2298
 |||||
 |

Db 661 GAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGAGCCAGTTCTCAGAAGAAAAGGAGCAA 720

Qy	2299	GAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAA	2358
Db	721	GAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAA	780
Qy	2359	CAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCA	2418
Db	781	CAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCA	840
Qy	2419	GAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAACGTAAATTAGGAACTGGGGAA	2478
Db	841	GAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAACGTAAATTAGGAACTGGGGAA	900
Qy	2479	ATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTACAGAAACAA	2538
Db	901	ATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTACAGAAACAA	960
Qy	2539	TTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGA	2598
Db	961	TTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGA	1020
Qy	2599	AAACTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAACGTGGCAACTGGACAAGAAGAGTTC	2658
Db	1021	AAACTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAACGTGGCAACTGGACAAGAAGAGTTC	1080
Qy	2659	AGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAA	2718
Db	1081	AGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAA	1140
Qy	2719	GCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAAAGTATG	2778
Db	1141	GCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAAAGTATG	1200
Qy	2779	GAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGA	2838
Db	1201	GAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGA	1260
Qy	2839	ATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAG	2898
Db	1261	ATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAG	1320
Qy	2899	GAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCT	2958
Db	1321	GAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCT	1380
Qy	2959	GATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGA	3018
Db	1381	GATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGA	1440
Qy	3019	ACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGC	3078
Db	1441	ACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGC	1500
Qy	3079	AGAAAGGCAGCACAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAACTCCTG	3138
Db	1501	AGAAAGGCAGCACAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAACTCCTG	1560
Qy	3139	CAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTA	3198
Db	1561	CAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTA	1620
Qy	3199	GGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATGGAACGA	3258

Db	1621		GGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAAACTGAATGAGACAATGGAACGA	1680
Qy	3259		CAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAA	3318
Db	1681		CAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAA	1740
Qy	3319		GGAGGCTTTGAAAATGTTTGTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAG	3378
Db	1741		GGAGGCTTTGAAAATGTTTGTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAG	1800
Qy	3379		AATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATG	3438
Db	1801		AATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATG	1860
Qy	3439		CCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGT	3498
Db	1861		CCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGT	1920
Qy	3499		GTTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAGCAGGAT	3558
Db	1921		GTTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAGCAGGAT	1980
Qy	3559		GGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGG	3618
Db	1981		GGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGG	2040
Qy	3619		AGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAA	3678
Db	2041		AGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAA	2100
Qy	3679		GAGAGTGAGCTGGATGACCAAGAAGAACCCCATTTGTGCCTCCTCCTGGATACATGATG	3738
Db	2101		GAGAGTGAGCTGGATGACCAAGAAGAACCCCATTTGTGCCTCCTCCTGGATACATGATG	2160
Qy	3739		TATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCT	3798
Db	2161		TATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCT	2220
Qy	3799		CCTCCCTTGCCAAACAATAGCCGACCTCTCACCCTGGCACTGTTGTTTATGGCCACCT	3858
Db	2221		CCTCCCTTGCCAAACAATAGCCGACCTCTCACCCTGGCACTGTTGTTTATGGCCACCT	2280
Qy	3859		CCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCAACTTCTCCATCCCTTCATC	3918
Db	2281		CCTGCTGGGGCCCC-----CCCCCAACTTCTCCATCCCTTCATC	2322
Qy	3919		CCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCT	3978
Db	2323		CCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCT	2382
Qy	3979		AGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGA	4038
Db	2383		AGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGA	2442
Qy	4039		GCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTT	4098
Db	2443		GCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTT	2502
Qy	4099		TTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACATAGAAGTGTCCAGAAA	4158

Db	2503	TTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACATAGAACTGTCCAGNNN	2562
Qy	4159	CGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAA	4218
Db	2563	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGAAATGTAGAGAGTCTTATGACTGAACTAGAA	2622
Qy	4219	ATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAG	4278
Db	2623	ATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAG	2682
Qy	4279	ACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAG	4338
Db	2683	ACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAG	2742
Qy	4339	AGTGAACCTTTCATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCAGTATGCC	4398
Db	2743	AGTGAACCTTTCATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCAGTATGCC	2802
Qy	4399	AAGAGAAGTTTATTGCAAACTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAA	4458
Db	2803	AAGAGAAGTTTATTGCAAACTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAA	2862
Qy	4459	ACTGCTGTAAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAG	4518
Db	2863	ACTGCTGTAAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAG	2922
Qy	4519	GATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTA	4578
Db	2923	GATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTA	2982
Qy	4579	GCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAG	4638
Db	2983	GCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAG	3042
Qy	4639	CTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAG	4698
Db	3043	CTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAG	3102
Qy	4699	GTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAA	4758
Db	3103	GTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAA	3162
Qy	4759	AGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAA	4818
Db	3163	AGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAA	3222
Qy	4819	AAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAA	4878
Db	3223	AAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAA	3282
Qy	4879	GCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAA	4938
Db	3283	GCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAA	3342
Qy	4939	TCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGA	4998
Db	3343	TCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGA	3402
Qy	4999	AAAACCTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTT	5058
Db	3403	AAAACCTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTT	3462

Qy	5059	GTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAATATTCTGGACATGTTGCAA	5118
Db	3463	GTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAATATTCTGGACATGTTGCAG	3522
Qy	5119	CTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGACCAAAGGGTATCTGAATTA	5178
Db	3523	CTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGACCAAAGGGTATCTGAATTA	3582
Qy	5179	GAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAGAATTTGCAGCAGATA	5238
Db	3583	GAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAGAATTTGCAGCAGATA	3642
Qy	5239	TCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTTGAGAGGGATAAACGA	5298
Db	3643	TCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTTGAGAGGGATAAACGA	3702
Qy	5299	GAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCGTGTGTTGAGTGTTTGAGC	5358
Db	3703	GAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCGTGTGTTGAGTGTTTGAGC	3762
Qy	5359	AAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAAAAAAAGTTGGCACAAACC	5418
Db	3763	AAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAAAAAAAGTTGGCACAAACC	3822
Qy	5419	AAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAATCAAACCTAGAAAAG	5478
Db	3823	AAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAATCAAACCTAGAAAAG	3882
Qy	5479	TTGGAATTGAATGTCAGAAAACCTGCAGCAGGAAGTAGACCAACTAAACAGAGACAAGTTG	5538
Db	3883	TTGGAATTGAATGTCAGAAAACCTGCAGCAGGAAGTAGACCAACTAAACAGAGACAAGTTG	3942
Qy	5539	TCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAAAAACGAGAAGCAGTA	5598
Db	3943	TCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAAAAACGAGAAGCAGTA	4002
Qy	5599	AACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTTGAACCTAGCAAAACAGGAC	5658
Db	4003	AACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTTGAACCTAGCAAAACAGGAC	4062
Qy	5659	CTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAG	5718
Db	4063	CTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAG	4122
Qy	5719	GACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTGAGAAAGAAGAGGAGACAAAACAA	5778
Db	4123	GACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTGAGAAAGAAGAGGAGACAAAACAA	4182
Qy	5779	CAACAACCTTCAAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTCAAACCTAGTCCAACAA	5838
Db	4183	CAACAACCTTCAAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTCAAACCTAGTCCAACAA	4242
Qy	5839	GAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAAAGCAAATTAGAAAACC	5898
Db	4243	GAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAAAGCAAATTAGAAAACC	4302
Qy	5899	AGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAA	5958
Db	4303	AGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAA	4362

Qy	5959	AGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTG	6018
Db	4363	AGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTG	4422
Qy	6019	CAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAAACATAACCGCAG	6078
Db	4423	CAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAAACATAACCGCAG	4482
Qy	6079	CTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCCTCCAGAAA	6138
Db	4483	CTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCCTCCAGAAA	4542
Qy	6139	GAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAGTTCTTGACAGAAAAGA	6198
Db	4543	GAGGCAGATTCTATGAGGGCAGACTTCNNNNNNNNNNNNNNNNNNNNCTTGACAGAAAAGA	4602
Qy	6199	AAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAGATCCAGCGGAGCCAG	6258
Db	4603	AAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAGATCCAGCGGAGCCAG	4662
Qy	6259	CTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATACAAAAGGAAATGGCA	6318
Db	4663	CTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATACAAAAGGAAATGGCA	4722
Qy	6319	ACAATTGAACTGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGCCTGATGAAGGAGCTC	6378
Db	4723	ACAATTGAACTGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGCCTGATGAAGGAGCTC	4782
Qy	6379	AACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATGGCAAACCAAAAGATTG	6438
Db	4783	AACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATGGCAAACCAAAAGATTG	4842
Qy	6439	GAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTTAAATCTGAGGTGAAGGAT	6498
Db	4843	GAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTTAAATCTGAGGTGAAGGAT	4902
Qy	6499	GAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAACTACCAGCAGATCTA	6558
Db	4903	GAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAACTACCAGCAGATCTA	4962
Qy	6559	GAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAAC	6618
Db	4963	GAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAAC	5022
Qy	6619	CTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTGAACTTTTCCCAAGTTCAC	6678
Db	5023	CTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTGAACTTTTCCCAAGTTCAC	5082
Qy	6679	ATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAACTGCGTCACCGGGAAGAC	6738
Db	5083	ATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAAACTGCGTCACCGGGAAGAC	5142
Qy	6739	CGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAGGA	6798
Db	5143	CGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAGGA	5202
Qy	6799	AAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTAGATGCTTTAGGGGAA	6858
Db	5203	AAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTAGATGCTTTAGGGGAA	5262
Qy	6859	TTGGTCACCAGCACCTCTGCAGATTTCAGCGTCATCACCCAGTCTGTCTCAGCTGGAGTCT	6918

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Db      5263 TTGGTCACCAGCACCTCTGCAGATTCAGCGTCATCACCCAGTCTGTCTCAGCTGGAGTCT 5322
Qy      6919 TCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA 6978
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5323 TCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA 5382

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RESULT 8

AAL51566

ID AAL51566 standard; DNA; 5902 BP.

XX

AC AAL51566;

XX

DT 10-APR-2003 (first entry)

XX

DE Human nucleic acid-associated protein coding sequence - SEQ ID No 49.

XX

KW Human; gene; ds; nucleic acid-associated protein; NAAP; arteriosclerosis;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS;
 KW cancer; developmental disorder; renal tubular acidosis; anaemia; asthma;
 KW mental retardation; neurological disorder; Alzheimer's disease; epilepsy;
 KW Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;
 KW Crohn's disease; transgenic animal; animal model.

XX

OS Homo sapiens.

XX

PN WO2003000864-A2.

XX

PD 03-JAN-2003.

XX

PF 20-JUN-2002; 2002WO-US021179.

XX

PR 22-JUN-2001; 2001US-0300518P.

PR 29-JUN-2001; 2001US-0301787P.

PR 29-JUN-2001; 2001US-0301792P.

PR 29-JUN-2001; 2001US-0301892P.

PR 29-JUN-2001; 2001US-0301893P.

PR 06-JUL-2001; 2001US-0303405P.

PR 06-JUL-2001; 2001US-0303442P.

PR 15-MAR-2002; 2002US-0364438P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM;

PI Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ;

PI Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR;

PI Borowsky ML, Yao MG, Walia NK, Bandman O, Lal PG, Becha SD, Lee SY;

PI Richardson TW, Elliott VS, Luo W, Tang YT, Zebarjadian Y, Lu Y;

XX

DR WPI; 2003-201420/19.

DR P-PSDB; AA016416.

XX

PT New nucleic acid-associated proteins and polynucleotides, useful for
 PT diagnosing, treating or preventing cell proliferative (e.g. cancer),
 PT neurological (e.g. epilepsy or Parkinson's disease), or autoimmune
 PT disorders (e.g. AIDS).

XX

PS Claim 12; Page 286-288; 312pp; English.

XX

CC The invention comprises the amino acid and coding sequences of human

CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
CC the invention are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of NAAP, such as: cell proliferative
CC disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis
CC or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia
CC or mental retardation); neurological disorders (e.g. Alzheimer's disease,
CC Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders
CC (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of
CC the invention are useful for creating transgenic animals to model human
CC disease. The present DNA sequence encodes a human nucleic acid-associated
CC protein of the invention

XX

SQ Sequence 5902 BP; 2088 A; 1130 C; 1486 G; 1198 T; 0 U; 0 Other;

Query Match 72.2%; Score 5034.8; DB 8; Length 5902;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 5187; Conservative 0; Mismatches 2; Indels 141; Gaps 1;

QY 1649 ATTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC 1708

Db 165 AGTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACACAGCTTGACATTATGAACAAGC 224

Qy 1709 AGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAAACGG 1768
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 225 AGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGG 284

Qy 1769 AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC 1828

Db 285 AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC 344

Qy 1829 TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG 1888

Db 345 TGAAGAAGGATTAGAAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG 404

Qy 1889 GCCAGGCAACTCAGGCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT 1948

Db 405 GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT 464

Qy 1949 TGCAGAGATTGACAGAAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG 2008

Db 465 TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG 524

Qy 209 CAGAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG 268

Db 525 CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG 584

Qy 2069 TGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGG 2128
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 585 TGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGG 644

Qy 2129 CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA 2188

Db 645 CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA 704

Qy 2189 CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG 2248

Db 705 CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG 764

Qy 2249 CCCTCAAGAATGCCCTTGGAAAAGCCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG 2308
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 765 CCCTCAAGAATGCCCTTGGAAAAGCCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG 824

Qy	2309	AGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAAACAGCAACTTA	2368
Db	825	AGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAAACAGCAACTTA	884
Qy	2369	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	2428
Db	885	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	944
Qy	2429	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTAAATTAGGAAGTGGGGAAATGAACATCC	2488
Db	945	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTAAATTAGGAAGTGGGGAAATGAACATCC	1004
Qy	2489	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	2548
Db	1005	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	1064
Qy	2549	TTCTTGCACGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAG	2608
Db	1065	TTCTTGCACGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAG	1124
Qy	2609	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCCT	2668
Db	1125	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCCT	1184
Qy	2669	GTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCC	2728
Db	1185	GTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCC	1244
Qy	2729	AGCAAATGGAGAATGAAATTCATATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCC	2788
Db	1245	AGCAAATGGAGAATGAAATTCATATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCC	1304
Qy	2789	AAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCCTGGCCC	2848
Db	1305	AAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCCTGGCCC	1364
Qy	2849	AACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTT	2908
Db	1365	AACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTT	1424
Qy	2909	TTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAG	2968
Db	1425	TTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAG	1484
Qy	2969	CCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAACTGTTATGA	3028
Db	1485	CCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAACTGTTATGA	1544
Qy	3029	AAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAG	3088
Db	1545	AAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAG	1604
Qy	3089	CACAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAACTCTCC	3148
Db	1605	CACAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAACTCTCC	1664
Qy	3149	TCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAG	3208
Db	1665	TCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAG	1724

Qy	3209	CAAAC	TACAGG	TCTAGAA	ATTGAGAA	ACTGAAT	GAGACA	AATGGA	ACGACAA	AGGACAG	3268
Db	1725	CAAAC	TACAGG	TCTAGAA	ATTGAGAA	ACTGAAT	GAGACA	AATGGA	ACGACAA	AGGACAG	1784
Qy	3269	AGATT	GCAAGG	CTGCAGA	ATGTACT	AGACCT	CACTGGA	AGTGACA	ACAAAGG	AGGCTTTG	3328
Db	1785	AGATT	GCAAGG	CTGCAGA	ATGTACT	AGACCT	CACTGGA	AGTGACA	ACAAAGG	AGGCTTTG	1844
Qy	3329	AAAAT	GTTTTA	GAGAAAT	TGCTGAA	CTTCGAC	GTGAAG	TTTCTT	ATCAGA	ATGATTACA	3388
Db	1845	AAAAT	GTTTTA	GAGAAAT	TGCTGAA	CTTCGAC	GTGAAG	TTTCTT	ATCAGA	ATGATTACA	1904
Qy	3389	TAAGC	AGCATG	GCAGAT	CCTTTCA	AAAAGAC	GAGGCT	ATTGGT	ACTTTAT	GCCACCACCAC	3448
Db	1905	TAAGC	AGCATG	GCAGAT	CCTTTCA	AAAAGAC	GAGGCT	ATTGGT	ACTTTAT	GCCACCACCAC	1964
Qy	3449	CATCAT	CAAAAG	TTTCCAG	CCATAGT	TCCCAGG	CCACCA	AGGACT	CTGGTGT	TGGCCTTA	3508
Db	1965	CATCAT	CAAAAG	TTTCCAG	CCATAGT	TCCCAGG	CCACCA	AGGACT	CTGGTGT	TGGCCTTA	2024
Qy	3509	AGTACT	CAGCCT	CAACTC	CTGTAG	AAAACCA	CGCCCT	TGGGCAG	CAGGATG	GGGAAGGAAG	3568
Db	2025	AGTACT	CAGCCT	CAACTC	CTGTAG	AAAACCA	CGCCCT	TGGGCAG	CAGGATG	GGGAAGGAAG	2084
Qy	3569	GCAGT	CAACCT	CCCCCT	GCCTCAG	GATACT	GGGTTT	TATTCT	CCCATC	AGGAGTGGGTTAC	3628
Db	2085	GCAGT	CAACCT	CCCCCT	GCCTCAG	GATACT	GGGTTT	TATTCT	CCCATC	AGGAGTGGGTTAC	2144
Qy	3629	ATAAA	CTGTTT	CCAAGT	AGAGAT	GCAGAC	AGTGG	AGGAGAT	AGTCAGG	AAGAGAGTGAGC	3688
Db	2145	ATAAA	CTGTTT	CCAAGT	AGAGAT	GCAGAC	AGTGG	AGGAGAT	AGTCAGG	AAGAGAGTGAGC	2204
Qy	3689	TGGAT	GACCA	AGAAGA	ACCCCC	ATTTGT	GCCTC	CTCCTG	GATACAT	GATGTATACTGTGC	3748
Db	2205	TGGAT	GACCA	AGAAGA	ACCCCC	ATTTGT	GCCTC	CTCCTG	GATACAT	GATGTATACTGTGC	2264
Qy	3749	TTCCT	GATGGT	TCTCCT	GTACCC	CAGGGC	ATGGCC	CTGTAT	GCACCAC	CTCCTCCCTTGC	3808
Db	2265	TTCCT	GATGGT	TCTCCT	GTACCC	CAGGGC	ATGGCC	CTGTAT	GCACCAC	CTCCTCCCTTGC	2324
Qy	3809	CAAAC	AATAGC	CGACCT	CTCACCC	CTGGCA	CTGTTG	TTTATG	GCCCAC	CTCCTGCTGGGG	3868
Db	2325	CAAAC	AATAGC	CGACCT	CTCACCC	CTGGCA	CTGTTG	TTTATG	GCCCAC	CTCCTGCTGGGG	2384
Qy	3869	CCCCC	ATGGT	GTATGG	GCCTCC	ACCCCC	CAACTT	CTCCAT	CCCCCT	CATCCCTATGGGTG	3928
Db	2385	CCCCC	ATGGT	GTATGG	GCCTCC	ACCCCC	CAACTT	CTCCAT	CCCCCT	CATCCCTATGGGTG	2444
Qy	3929	TGCTG	CATTG	CAACGT	CCCTGA	ACACC	ATAACT	TAGAGA	ATGAAG	TTTCTAGATTAGAAG	3988
Db	2445	TGCTG	CATTG	CAACGT	CCCTGA	ACACC	ATAACT	TAGAGA	ATGAAG	TTTCTAGATTAGAAG	2504
Qy	3989	ACATA	ATGCAG	CATTTA	AAATCAA	AGAAG	CGGGA	AAGAA	AGGTGG	ATGAGAGCATCCAAGC	4048
Db	2505	ACATA	ATGCAG	CATTTA	AAATCAA	AGAAG	CGGGA	AAGAA	AGGTGG	ATGAGAGCATCCAAGC	2564
Qy	4049	GGCAG	TCGGAG	AAAGAA	ATGGA	AGAACT	GCATCA	TAAATAT	TGATGAT	CTTTTGCAAGAGA	4108
Db	2565	GGCAG	TCGGAG	AAAGAA	ATGGA	AGAACT	GCATCA	TAAATAT	TGATGAT	CTTTTGCAAGAGA	2624
Qy	4109	AGAAA	AGCTT	AGAGTG	TGAAGT	AGAGA	ATTACA	TAGAACT	GTCCAGA	AACGTCAACAGC	4168

Db	2625	 AGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACATAGAAGTGTCCAGAAACGTCAACAGC	2684
Qy	4169	AAAAGGACTTCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAAATAGAAAAAT	4228
Db	2685	 AAAAGGACTTCATTGATGGAAATGTAGAGAGTCTTATGACTGAACTAGAAAATAGAAAAAT	2744
Qy	4229	CACTCAAACATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGA	4288
Db	2745	 CACTCAAACATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGA	2804
Qy	4289	AACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTT	4348
Db	2805	 AACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTT	2864
Qy	4349	CATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCAC TGATGCCAAGAGAAAGTT	4408
Db	2865	 CATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCAC TGATGCCAAGAGAAAGTT	2924
Qy	4409	TATTGCAAAC TGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAACTGCTGTTA	4468
Db	2925	 TATTGCAAAC TGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAACTGCTGTTA	2984
Qy	4469	ACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGC	4528
Db	2985	 ACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGC	3044
Qy	4529	AGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAAG	4588
Db	3045	 AGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAAG	3104
Qy	4589	ACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAAACTGACAGAAGAGCTTCAGAAAC	4648
Db	3105	 ACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAAACTGACAGAAGAGCTTCAGAAAC	3164
Qy	4649	TACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAGGTCTTAAAG	4708
Db	3165	 TACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAGGTCTTAAAG	3224
Qy	4709	AATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGA	4768
Db	3225	 AATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGA	3284
Qy	4769	CAAGTCAGCAGCAGGAGATGGCTGTCTTGACAGGCAGTTAGGGCATAAAAAGGAGGAGC	4828
Db	3285	 CAAGTCAGCAGCAGGAGATGGCTGTCTTGACAGGCAGTTAGGGCATAAAAAGGAGGAGC	3344
Qy	4829	TGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAAGCTCTGAGAC	4888
Db	3345	 TGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAAGCTCTGAGAC	3404
Qy	4889	TGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAATCTCTTCTGG	4948
Db	3405	 TGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAATCTCTTCTGG	3464
Qy	4949	AAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAAC	5008
Db	3465	 AAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAAC	3524
Qy	5009	TTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAATCTTCAGGTTGTTTAAAGGC	5068

Db	3525	TTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTTGTTTTAAGGC	3584
Qy	5069	AGATGTCTAAACATAAAACCGAACTAAAGAATATTCTGGACATGTTGCAACTTGAAAACC	5128
Db	3585	AGATGTCTAAACATAAAACCGAACTAAAGAATATTCTGGACATGTTGCAACTTGAAAACC	3644
Qy	5129	ATGAGCTACAAGGTTTGAAGCTACAACATGACCAAAGGGTATCTGAATTAGAGAAGACTC	5188
Db	3645	ATGAGCTACAAGGTTTGAAGCTACAACATGACCAAAGGGTATCTGAATTAGAGAAGACTC	3704
Qy	5189	AGGTGGCAGTGCTAGAGGAGAAACTGGAGTTAGAGAATTTGCAGCAGATATCCCAGCAGC	5248
Db	3705	AGGTGGCAGTGCTAGAGGAGAAACTGGAGTTAGAGAATTTGCAGCAGATATCCCAGCAGC	3764
Qy	5249	AGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTTGAGAGGGATAAACGAGAAATAGAAC	5308
Db	3765	AGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTTGAGAGGGATAAACGAGAAATAGAAC	3824
Qy	5309	GAATGACTGCTGAGTCCCGAGCTTTACAATCGTGTGTTGAGTGTGTTGAGCAAAGAAAAGG	5368
Db	3825	GAATGACTGCTGAGTCCCGAGCTTTACAATCGTGTGTTGAGTGTGTTGAGCAAAGAAAAGG	3884
Qy	5369	AAGATCTCCAAGAGAAATGTGACATTTGGGAAAAAAAGTTGGCACAACCAAAAGGGTTT	5428
Db	3885	AAGATCTCCAAGAGAAATGTGACATTTGGGAAAAAAAGTTGGCACAACCAAAAGGGTTT	3944
Qy	5429	TAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAATCAAACCTAGAAAAGTTGGAATTGA	5488
Db	3945	TAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAATCAAACCTAGAAAAGTTGGAATTGA	4004
Qy	5489	ATGTCAGAAAACGTCAGCAGGAACTAGACCAACTAAACAGAGACAAGTTGTCACTGCATA	5548
Db	4005	ATGTCAGAAAACGTCAGCAGGAACTAGACCAACTAAACAGAGACAAGTTGTCACTGCATA	4064
Qy	5549	ACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAAAAACGAGAAGCAGTAAACTCACTGC	5608
Db	4065	ACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAAAAACGAGAAGCAGTAAACTCACTGC	4124
Qy	5609	AGGAGGAAC TAGCTAATGTCCAAGACCATTTGAACCTAGCAAAACAGGACCTGCTTCACA	5668
Db	4125	AGGAGGAAC TAGCTAATGTCCAAGACCATTTGAACCTAGCAAAACAGGACCTGCTTCACA	4184
Qy	5669	CCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTG	5728
Db	4185	CCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTG	4244
Qy	5729	AATGGGCAAATAGGTTTGAAGACTGTGAGAAAGAGAGACAAAACAACAACAACTTC	5788
Db	4245	AATGGGCAAATAGGTTTGAAGACTGTGAGAAAGAGAGACAAAACAACAACAACTTC	4304
Qy	5789	AAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGT	5848
Db	4305	AAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGT	4364
Qy	5849	TTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAAAGCAAATTAGAAACCAAGTAAAGTGA	5908
Db	4365	TTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAAAGCAAATTAGAAACCAAGTAAAGTGA	4424
Qy	5909	CACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGG	5968
Db	4425	CACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAACCTGG	4484

Qy	5969	ACCAAGTGTCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGG	6028
Db	4485	ACCAAGTGTCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGG	4544
Qy	6029	AGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAAATAAACGGCAGCTTTCAGAAA	6088
Db	4545	AGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAAATAAACGGCAGCTTTCAGAAA	4604
Qy	6089	GGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATT	6148
Db	4605	GGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCCTCCAGAAAGAGGCAGATT	4664
Qy	6149	CTATGAGGGCAGACTTCAGCCTTCTGCGGAACAGTTCTTGACAGAAAGAAAGAAAGCTG	6208
Db	4665	CTATGAGGGCAGACTTCAGCCTTCTGCGGAACAGTTCTTGACAGAAAGAAAGAAAGCTG	4724
Qy	6209	AGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAA	6268
Db	4725	AGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAGATCCAGCGGAGCCAGCTGGAGAAAA	4784
Qy	6269	ACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATACAAAAGGAAATGGCAACAATTGAAC	6328
Db	4785	ACCTTCTT-----	4792
Qy	6329	TGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGCCTGATGAAGGAGCTCAACCAGATGC	6388
Db	4793	-----	4792
Qy	6389	AGTATGAGTACACGGAGCTCAAGAAACAGATGGCAAACCAAAAAGATTTGGAGAGAAGAC	6448
Db	4793	-----ATGGCAAACCAAAAAGATTTGGAGAGAAGAC	4823
Qy	6449	AAATGGAAATCAGTGATGCAATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAA	6508
Db	4824	AAATGGAAATCAGTGATGCAATGAGGACACTTAAATCTGAGGTGAAGGATGAAATCAGAA	4883
Qy	6509	CCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTT	6568
Db	4884	CCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTT	4943
Qy	6569	TGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTA	6628
Db	4944	TGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTA	5003
Qy	6629	CCATGAATGAGGGACCTTTTGAAGAAAACTGAACTTTTCCCAAGTTCACATAATGGATG	6688
Db	5004	CCATGAATGAGGGACCTTTTGAAGAAAACTGAACTTTTCCCAAGTTCACATAATGGATG	5063
Qy	6689	AACACTGGCGTGGAGAAGCACTCCGGGAGAACTGCGTCACCGGGAAGACCGACTCAAGG	6748
Db	5064	AACACTGGCGTGGAGAAGCACTCCGGGAGAACTGCGTCACCGGGAAGACCGACTCAAGG	5123
Qy	6749	CCCAACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGA	6808
Db	5124	CCCAACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAAGGAAAGCGGCAGA	5183
Qy	6809	CAGAGGGCACTTTACACAGTTTGAAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCA	6868
Db	5184	CAGAGGGCACTTTACACAGTTTGAAGGAGACAAGTAGATGCTTTAGGGGAATTGGTCACCA	5243

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Qy      6869 GCACCTCTGCAGATTCAGCGTCATCACCCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAG 6928
          |||
Db      5244 GCACCTCTGCAGATTCAGCGTCATCACCCAGTCTGTCTCAGCTGGAGTCTTCCCTCACAG 5303

Qy      6929 AGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA 6978
          |||
Db      5304 AGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA 5353

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RESULT 9

ADR07863

ID ADR07863 standard; cDNA; 3602 BP.

XX

AC ADR07863;

XX

DT 04-NOV-2004 (first entry)

XX

DE Full length human cDNA useful for treating neurological disease Seq 1369.

XX

KW gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;

KW osteoporosis; neurological disease; Alzheimer's disease;

KW Parkinson's disease; dementia; short memory; cancer;

KW sense or motor function; emotional reaction; fear response; panic;

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

KW tranquiliser.

XX

OS Homo sapiens.

XX

PN EP1447413-A2.

XX

PD 18-AUG-2004.

XX

PF 12-FEB-2004; 2004EP-00003145.

XX

PR 14-FEB-2003; 2003JP-00102207.

PR 09-MAY-2003; 2003JP-00131452.

XX

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;

PI Wakamatsu A, Ishii S, Nagai K, Irie R;

XX

DR WPI; 2004-583265/57.

DR P-PSDB; ADR09819.

XX

PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX

PS Claim 1; SEQ ID NO 1369; 2686pp; English.

XX

CC This invention relates to novel, isolated full length human cDNA

CC molecules and the encoded proteins thereof. Specifically, it refers to

CC cDNA clones obtained by an oligo-capping method, where none of these

CC clones are identical to any known human mRNAs. The present invention

CC describes an immunoassay to identify agonists and antagonists, as well as

CC antibodies, antisense molecules and siRNAs that can all be used to bind

CC to and modulate expression of the cDNA molecules. As such, these

CC molecules are useful for diagnostic markers or therapeutic targets for

CC the various diseases or morbid states. In particular, they are useful in

CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's

CC disease, Parkinson's disease, dementia, short memory and various cancers,

CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cytostatic and tranquiliser activities. This polynucleotide is a full
CC length human cDNA sequence of the invention. NOTE: This sequence is not
CC given in the sequence listing of the specification but can be obtained on
CC CD-ROM from the European Patent Office, Vienna Sub-office.

XX

SQ Sequence 3602 BP; 1284 A; 712 C; 859 G; 747 T; 0 U; 0 Other;

Query Match 51.6%; Score 3597.4; DB 13; Length 3602;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 459 CTTATCATATAACAAAATCAGCAAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAA 518
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 4 CTTATCATATAACAAAATCAGCAAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAA 63

Qy 519 GCTTAACCTTGCAGGAAATGAAATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAA 578
|||

Db 64 GCTTAACCTTGCAGGAAATGAAATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAA 123

Qy 579 ATCTTTGCGAGTCCTCAATTTGAAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAA 638

Db 124 ATCTTTGCGAGTCCTCAATTTGAAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAA 183

Qy 639 GTTGAAACCGCTTCAAGATTTGATTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCT 698

Db 184 GTTGAAACTGCTTCAAGATTTGATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCT 243

Qy 699 TCCTCATTACCTCCAGTTTACCATTTTCCACCTCCGTTTCATTGGAAAGTTTGGAAAGGTCA 758

Db 244 TCCTCATTACCTCCAGTTTACCATTTTCCACCTCCGTTTCATTGGAAAGTTTGGAAGGTCA 303

Qy 759 GCCAGTAACCACTCAGGATAGACAGGAGGCTTTTGAGAGATTTCAGTTTAGAAGAGGTAGA 818

Db 304 GCCAGTAACCACTCAGGATAGACAGGAGGCTTTTGAGAGATTCAGTTTAGAAGAGGTAGA 363

Qy 819 AAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACA 878

Db 364 AAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACA 423

Qy 879 AACAAAGGTTCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCATTAAAAAGAGGA 938

Db 424 AACAAAGGTTCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGA 483

Qy 939 GGCCATGTTACAGAAACAGAGCTGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGA 998

Db 484 GGCCATGTTACAGAAACAGAGCTGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGA 543

Qy 999 ATTGCTAA AACAGAA GACCATAG AATTAAC ACAGAGCAT GTCTAGA AGCAATAT GAGCTGGA 1058

Db 544 ATTGCTAAACAGAAGACCATAGAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGA 603

Qy 1059 ACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAATTATTATCCATC 1118
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 604 ACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAATTATTATCCATC 663

Qy 1119 AGAGTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATA 1178
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 664 AGAGTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATA 723

Qy	1179	CAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGAT	1238
Db	724	CAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGAT	783
Qy	1239	CAAGAAGATGGAGCCAGATGAACAACTTAGAAATGATCACATGAACTTGAGAGGCCACAC	1298
Db	784	CAAGAAGATGGAGCCAGATGAACAACTTAGAAATGATCACATGAACTTGAGAGGCCACAC	843
Qy	1299	ACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCACAACTCGACT	1358
Db	844	ACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCACAACTCGACT	903
Qy	1359	ATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAACTTTTGAGAGCTACTGAAGA	1418
Db	904	ATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAACTTTTGAGAGCTACTGAAGA	963
Qy	1419	ATTTAAACAACTGGAAGAAGCTATACAACATAAAAAAGATTTTTCAGAACGAGGAAAGACCT	1478
Db	964	ATTTAAACAACTGGAAGAAGCTATACAACATAAAAAAGATTTTTCAGAACGAGGAAAGACCT	1023
Qy	1479	TCTTTACAAGCAGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCT	1538
Db	1024	TCTTTACAAGCAGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCT	1083
Qy	1539	GGATCTAGAAGTGCAGATGGAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGAT	1598
Db	1084	GGATCTAGAAGTGCAGATGGAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGAT	1143
Qy	1599	TAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATAT	1658
Db	1144	TAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATAT	1203
Qy	1659	GAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAACA	1718
Db	1204	GAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAACA	1263
Qy	1719	ACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAA	1778
Db	1264	ACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAA	1323
Qy	1779	GGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGA	1838
Db	1324	GGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGA	1383
Qy	1839	TTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAAC	1898
Db	1384	TTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAAC	1443
Qy	1899	TCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATT	1958
Db	1444	TCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATT	1503
Qy	1959	GACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATAT	2018
Db	1504	GACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATAT	1563
Qy	2019	GAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATC	2078
Db	1564	GAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATC	1623

Qy	2079	TTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAA	2138
Db	1624	TTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAA	1683
Qy	2139	CCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTAC	2198
Db	1684	CCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTAC	1743
Qy	2199	CCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAA	2258
Db	1744	CCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAA	1803
Qy	2259	TGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGC	2318
Db	1804	TGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGC	1863
Qy	2319	AAAACCTTAAACACTTGCAGGATGACAATAATCTGTTAAAACAGCAACTTAAAGATTTC	2378
Db	1864	AAAACCTTAAACACTTGCAGGATGACAATAATCTGTTAAAACAGCAACTTAAAGATTTC	1923
Qy	2379	GAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGT	2438
Db	1924	GAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGT	1983
Qy	2439	GGATGAGCTAAGAAGAAAAGTAACTGAAATTAGGAACTGGGGAATGAACATCCATAGTCTTC	2498
Db	1984	GGATGAGCTAAGAAGAAAAGTAACTGAAATTAGGAACTGGGGAATGAACATCCATAGTCTTC	2043
Qy	2499	AGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCTTGACAG	2558
Db	2044	AGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCTTGACAG	2103
Qy	2559	CTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGAAAACCTCCAAGAAGAAATGGC	2618
Db	2104	CTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGAAAACCTCCAAGAAGAAATGGC	2163
Qy	2619	TCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTTCAGGCAGGCCTGTGAGAGAGC	2678
Db	2164	TCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTTCAGGCAGGCCTGTGAGAGAGC	2223
Qy	2679	CCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGA	2738
Db	2224	CCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGA	2283
Qy	2739	GAATGAAATTCACCTATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTAC	2798
Db	2284	GAATGAAATTCACCTATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTAC	2343
Qy	2799	AGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGA	2858
Db	2344	AGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGA	2403
Qy	2859	GTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGA	2918
Db	2404	GTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGA	2463
Qy	2919	TAAAGAACTGAAGAACTTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGA	2978
Db	2464	TAAAGAACTGAAGAACTTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGA	2523
Qy	2979	GCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCA	3038

Db	2524	 GCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGAAAAATTAACCA	2583
Qy	3039	GGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGC	3098
Db	2584	 GGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGC	2643
Qy	3099	CAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAA	3158
Db	2644	 CAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAA	2703
Qy	3159	GGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAATCACA	3218
Db	2704	 GGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAATCACA	2763
Qy	3219	GGTCCTAGAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCAAG	3278
Db	2764	 GGTCCTAGAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCAAG	2823
Qy	3279	GCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTT	3338
Db	2824	 GCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTT	2883
Qy	3339	AGAAGAAATTGCTGAACCTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCAT	3398
Db	2884	 AGAAGAAATTGCTGAACCTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCAT	2943
Qy	3399	GGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCAA	3458
Db	2944	 GGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCAA	3003
Qy	3459	AGTTTCCAGCCATAGTTCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGC	3518
Db	3004	 AGTTTCCAGCCATAGTTCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGC	3063
Qy	3519	CTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACC	3578
Db	3064	 CTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACC	3123
Qy	3579	TCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTT	3638
Db	3124	 TCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTT	3183
Qy	3639	TCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCA	3698
Db	3184	 TCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCA	3243
Qy	3699	AGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGG	3758
Db	3244	 AGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGG	3303
Qy	3759	TTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAG	3818
Db	3304	 TTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAG	3363
Qy	3819	CCGACCTCTACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGT	3878
Db	3364	 CCGACCTCTACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGT	3423
Qy	3879	GTATGGGCCTCCACCCCCCAACTTCTCCATCCCTTCATCCCTATGGGTGTGCTGCATTG	3938

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Db      3424 GTATGGGCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTG 3483
Qy      3939 CAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCA 3998
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3484 CAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCA 3543
Qy      3999 GCATTTAAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGG 4057
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3544 GCATTTAAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGG 3602

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RESULT 10

AEF74782

ID AEF74782 standard; DNA; 3893 BP.

XX

AC AEF74782;

XX

DT 06-APR-2006 (first entry)

XX

DE Human polynucleotide #296.

XX

KW Diagnosis; gene regulation; gene expression;

KW post traumatic stress disorder; psychiatric disorder; tranquilizer; gene;
KW ds.

XX

OS Homo sapiens.

XX

PN WO2006013561-A2.

XX

PD 09-FEB-2006.

XX

PF 02-AUG-2005; 2005WO-IL000824.

XX

PR 02-AUG-2004; 2004US-0592408P.

XX

PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.

XX

PI Segman R, Shalev A, Goltser T, Friedman N, Shefi N, Kaminski N;

XX

DR WPI; 2006-145797/15.

XX

PT New kit comprising 10 and no more than 574 polynucleotides capable of
 PT specifically binding at least one specific polynucleotide sequence,
 PT useful for determining predisposition of a subject to develop PTSD, or
 PT for diagnosing PTSD.

XX

PS Claim 1; SEQ ID NO 296; 157pp; English.

XX

CC The invention relates to a kit for determining predisposition of a
 CC subject to developing post-traumatic stress disorder (PTSD) comprising at
 CC least 10 and no more than 574 polynucleotides, where each of the
 CC polynucleotides is capable of specifically binding at least one specific
 CC polynucleotide sequence. The invention also relates to a kit for
 CC diagnosing PTSD in a subject, agents for the manufacture of the kits
 CC cited comprising the polynucleotides cited, and a microarray comprising
 CC at least 10 and no more than 904 oligonucleotides where each of the
 CC oligonucleotides is capable of specifically binding at least one specific
 CC polynucleotide sequence. The kit comprises each of the polynucleotides
 CC selected from an oligonucleotide molecule, a cDNA molecule, a genomic
 CC molecule and an RNA molecule. Each of the polynucleotides is at least 10

CC and no more than 50 nucleic acids in length. Each of the polynucleotides
 CC is bound to a solid support. The kit also comprises at least one reagent
 CC suitable for detecting hybridization of the polynucleotides and at least
 CC one RNA transcript. The kit further comprises packaging materials
 CC packaging the at least one reagent and instructions for using the kit in
 CC determining predisposition of the subject to developing PTSD, or for
 CC diagnosing the disease. The microarray comprises oligonucleotides of at
 CC least 10 and no more than 40 nucleic acids in length. The agent is
 CC capable of regulating an expression level of at least one gene as a
 CC pharmaceutical or for the manufacture of a medicament identified for
 CC preventing PTSD. The kit is useful for determining predisposition of a
 CC subject to developing PTSD or for diagnosing PTSD. This sequence
 CC represents a human polynucleotide of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 3893 BP; 1394 A; 732 C; 901 G; 866 T; 0 U; 0 Other;

Query Match 43.1%; Score 3008.6; DB 15; Length 3893;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3011; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	3964	GAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAAATCAAAGAAGCGGGAA	4023
Db	443	GAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAAATCAAAGAAGCGGGAA	502
Qy	4024	GAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCATCAT	4083
Db	503	GAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCATCAT	562
Qy	4084	AATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACAT	4143
Db	563	AATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACAT	622
Qy	4144	AGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGTCTT	4203
Db	623	AGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGTCTT	682
Qy	4204	ATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAAATT	4263
Db	683	ATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAAATT	742
Qy	4264	GAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTC	4323
Db	743	GAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTC	802
Qy	4324	CTGGCAGAGGCTGAGAGTGAACCTTCATGCACTAAAGAAAAGACAAAAATGCTGTTGAA	4383
Db	803	CTGGCAGAGGCTGAGAGTGAACCTTCATGCACTAAAGAAAAGACAAAAATGCTGTTGAA	862
Qy	4384	AAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTAGAA	4443
Db	863	AAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTAGAA	922
Qy	4444	AGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTC	4503
Db	923	AGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTC	982
Qy	4504	CAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAA	4563

Db	983	CAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAA	1042
Qy	4564	ATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAA	4623
Db	1043	ATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAA	1102
Qy	4624	AAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAG	4683
Db	1103	AAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAG	1162
Qy	4684	GATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAG	4743
Db	1163	GATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAG	1222
Qy	4744	CTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGACAGG	4803
Db	1223	CTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGACAGG	1282
Qy	4804	CAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCCAAAA	4863
Db	1283	CAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCCAAAA	1342
Qy	4864	GCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAAGTGAAGTGCAATCAC	4923
Db	1343	GCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAAGTGAAGTGCAATCAC	1402
Qy	4924	ATTAGGGAAGTAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTT	4983
Db	1403	ATTAGGGAAGTAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTT	1462
Qy	4984	CAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAA	5043
Db	1463	CAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAA	1522
Qy	5044	GAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAATATT	5103
Db	1523	GAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTACAGAATATT	1582
Qy	5104	CTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGACCAA	5163
Db	1583	CTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGACCAA	1642
Qy	5164	AGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAG	5223
Db	1643	AGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAG	1702
Qy	5224	AATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTT	5283
Db	1703	AATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTT	1762
Qy	5284	GAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCGTGT	5343
Db	1763	GAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCGTGT	1822
Qy	5344	GTTGAGTGTTTGTAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAAAAA	5403
Db	1823	GTTGAGTGTTTGTAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAAAAA	1882
Qy	5404	AAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAA	5463
Db	1883	AAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAA	1942

Qy	5464	TCAAACCTTAGAAAAGTTGGAATTGAATGTCAGAAAAGTGCAGCAGGAAGTAGACCAACTA	5523
Db	1943	TCAAACCTTAGAAAAGTTGGATTGAATGTCAGAAAAGTGCAGCAGGAAGTAGACCAACTA	2002
Qy	5524	AACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAA	5583
Db	2003	AACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAA	2062
Qy	5584	AAACGAGAAGCAGTAAACTCACTGCAGGAGGAAGTAGCTAATGTCCAAGACCATTGTAAC	5643
Db	2063	AAACGAGAAGCAGTAAACTCACTGCAGGAGGAAGTAGCTAATGTCCAAGACCATTGTAAC	2122
Qy	5644	CTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAG	5703
Db	2123	CTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAG	2182
Qy	5704	ACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAAGAA	5763
Db	2183	ACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAAGAA	2242
Qy	5764	GAGGAGACAAAACAACAACAACCTTCAAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTC	5823
Db	2243	GAGGAGACAAAACAACAACAACCTTCAAGTGCTTCAGAATGAGATTGAAGAAAACAAGCTC	2302
Qy	5824	AACTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAA	5883
Db	2303	AACTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAA	2362
Qy	5884	AGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAA	5943
Db	2363	AGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAA	2422
Qy	5944	TTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAG	6003
Db	2423	TTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAG	2482
Qy	6004	CGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCC	6063
Db	2483	CGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCC	2542
Qy	6064	CAAATAAACGGCAGCTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTG	6123
Db	2543	CAAATAAACGGCAGCTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTG	2602
Qy	6124	TTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAG	6183
Db	2603	TTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAG	2662
Qy	6184	TTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAG	6243
Db	2663	TTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAG	2722
Qy	6244	ATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATA	6303
Db	2723	ATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATA	2782
Qy	6304	CAAAGGAAATGGCAACAATTGAACTGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGC	6363
Db	2783	CAAAGGAAATGGCAACAATTGAACTGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGC	2842

```
Qy      6364 CTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATGGCA 6423
        |||
Db      2843 CTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATGGCA 2902

Qy      6424 AACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTTAAA 6483
        |||
Db      2903 AACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTTAAA 2962

Qy      6484 TCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAA 6543
        |||
Db      2963 TCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAA 3022

Qy      6544 CTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAA 6603
        |||
Db      3023 CTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAA 3082

Qy      6604 AGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTGAAC 6663
        |||
Db      3083 AGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTGAAC 3142

Qy      6664 TTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAACTG 6723
        |||
Db      3143 TTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAACTG 3202

Qy      6724 CGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCAGAA 6783
        |||
Db      3203 CGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCAGAA 3262

Qy      6784 GTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTA 6843
        |||
Db      3263 GTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTA 3322

Qy      6844 GATGCTTTAGGGGAATTGGTCAACCAGCACCTCTGCAGATTTCAGCGTCATCACCCAGTCTG 6903
        |||
Db      3323 GATGCTTTAGGGGAATTGGTCAACCAGCACCTCTGCAGATTTCAGCGTCATCACCCAGTCTG 3382

Qy      6904 TCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTGGACAAAATCAGGAAAAGAAT 6963
        |||
Db      3383 TCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTGGACAAAATCAGGAAAAGAAT 3442

Qy      6964 GCCTCAGCCAGATGA 6978
        |||
Db      3443 GCCTCAGCCAGATGA 3457
```

RESULT 11

ADM03364

ID ADM03364 standard; cDNA; 3044 BP.

XX

AC ADM03364;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human cDNA of the invention SEQ ID NO:2049.

XX

KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

XX

PN EP1347046-A1.

XX

PD 24-SEP-2003.
 XX
 PF 12-APR-2002; 2002EP-00008400.
 XX
 PR 22-MAR-2002; 2002JP-00137785.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-723558/69.
 DR P-PSDB; ADM05807.
 XX
 PT New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX
 PS Claim 1; SEQ ID NO 2049; 305pp; English.
 XX
 CC The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC cDNA sequence of the invention.
 XX
 SQ Sequence 3044 BP; 1050 A; 624 C; 735 G; 635 T; 0 U; 0 Other;

Query Match 41.2%; Score 2873.6; DB 11; Length 3044;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2876; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1093 TTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAA 1152
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 TTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAA 60
 Qy 1153 AGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATT 1212
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATT 120
 Qy 1213 ATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACTTAGAAAT 1272
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACTTAGAAAT 180
 Qy 1273 GATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAA 1332
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAA 240
 Qy 1333 AAAATAAGTGCAGCACAAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAA 1392
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 AAAATAAGTGCAGCACAAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAA 300
 Qy 1393 CAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACTAAAA 1452
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 CAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACTAAAA 360

Qy	1453	AAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTT	1512
Db	361	AAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTT	420
Qy	1513	GTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAG	1572
Db	421	GTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAG	480
Qy	1573	GAAATTGCCGGAAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGAT	1632
Db	481	GAAATTGCCGGAAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGAT	540
Qy	1633	TCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTT	1692
Db	541	TCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTT	600
Qy	1693	GACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGA	1752
Db	601	GACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGA	660
Qy	1753	ATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATA	1812
Db	661	ATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATA	720
Qy	1813	GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATAC	1872
Db	721	GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATAC	780
Qy	1873	CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	1932
Db	781	CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	840
Qy	1933	GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	1992
Db	841	GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	900
Qy	1993	ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAAGAGCTAGAAAGTGCCCTC	2052
Db	901	ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAAGAGCTAGAAAGTGCCCTC	960
Qy	2053	CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	2112
Db	961	CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	1020
Qy	2113	GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	2172
Db	1021	GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	1080
Qy	2173	GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	2232
Db	1081	GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	1140
Qy	2233	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAG	2292
Db	1141	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAG	1200
Qy	2293	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAAGGATGACAATAATCTG	2352
Db	1201	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAAGGATGACAATAATCTG	1260

Qy	2353	TTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	2412
Db	1261	TTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	1320
Qy	2413	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAACTGAAATTAGGAACT	2472
Db	1321	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAACTGAAATTAGGAACT	1380
Qy	2473	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAG	2532
Db	1381	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAG	1440
Qy	2533	AAACAATTCAGTGAAATTCCTGCACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGA	2592
Db	1441	AAACAATTCAGTGAAATTCCTGCACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGA	1500
Qy	2593	GAGAGAAACTCCAAGAAGAAATGGCTCTGCAGCAAGAGAACTGGCAACTGGACAAGAA	2652
Db	1501	GAGAGAAACTCCAAGAAGAAATGGCTCTGCAGCAAGAGAACTGGCAACTGGACAAGAA	1560
Qy	2653	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	2712
Db	1561	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	1620
Qy	2713	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	2772
Db	1621	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	1680
Qy	2773	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAATTCAGGAAGCTGATGAAGAGAAG	2832
Db	1681	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAATTCAGGAAGCTGATGAAGAGAAG	1740
Qy	2833	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	2892
Db	1741	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	1800
Qy	2893	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCC	2952
Db	1801	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCC	1860
Qy	2953	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	3012
Db	1861	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	1920
Qy	3013	CATGGAACGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	3072
Db	1921	CATGGAACGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	1980
Qy	3073	TTCAGCAGAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAA	3132
Db	1981	TTCAGCAGAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAA	2040
Qy	3133	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	3192
Db	2041	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	2100
Qy	3193	GGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	3252
Db	2101	GGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	2160
Qy	3253	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	3312

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Db      2161 GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC 2220
      |||
Qy      3313 AACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCT 3372
      |||
Db      2221 AACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCT 2280
      |||
Qy      3373 TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC 3432
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Db      2281 TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC 2340
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Qy      3433 TTTATGCCACCACCACCATCATCAAAAGTTTCAGCCATAGTTCCCAGGCCACCAAGGAC 3492
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Db      2341 TTTATGCCACCACCACCATCATCAAAAGTTTCAGCCATAGTTCCCAGGCCACCAAGGAC 2400
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Qy      3493 TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAG 3552
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Db      2401 TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAG 2460
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Qy      3553 CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC 3612
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Db      2461 CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC 2520
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Qy      3613 ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT 3672
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Qy      3673 CAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATAC 3732
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Db      2581 CAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATAC 2640
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Qy      3733 ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA 3792
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Db      2641 ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA 2700
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Qy      3793 CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGC 3852
      |||
Db      2701 CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGC 2760
      |||
Qy      3853 CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCC 3912
      |||
Db      2761 CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCC 2820
      |||
Qy      3913 TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAA 3972
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Db      2821 TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGTAAGTGGA 2880

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RESULT 12

AEC86294

ID AEC86294 standard; cDNA; 3044 BP.

XX

AC AEC86294;

XX

DT 01-DEC-2005 (first entry)

XX

DE Human cDNA clone TESTI20305540, SEQ ID 2049.

XX

KW Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;

KW Antiulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;

KW stomach ulcer; gastrointestinal ulcer; gene; ss.

XX
 OS Homo sapiens.
 XX
 PN EP1580263-A1.
 XX
 PD 28-SEP-2005.
 XX
 PF 12-APR-2002; 2004EP-00027348.
 XX
 PR 22-MAR-2002; 2002JP-00137785.
 PR 12-APR-2002; 2002EP-00008400.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2005-667421/69.
 DR P-PSDB; AEC88737.
 XX
 PT New full-length cDNA sequences, useful for treating diseases, e.g.
 PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
 XX
 PS Example 3; SEQ ID NO 2049; 296pp; English.
 XX
 CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)
 CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
 CC the functions of the proteins, and for developing medicines for diseases
 CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
 CC ulcer. Note: The sequence data for this patent did not form part of the
 CC printed specification but was obtained in electronic format directly from
 CC EPO.
 XX
 SQ Sequence 3044 BP; 1050 A; 624 C; 735 G; 635 T; 0 U; 0 Other;

Query Match 41.2%; Score 2873.6; DB 14; Length 3044;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2876; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1093 TTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAA 1152
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 Db 1 TTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAA 60

 Qy 1153 AGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATT 1212
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 Db 61 AGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATT 120

 Qy 1213 ATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACTTAGAAAT 1272
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACTTAGAAAT 180

 Qy 1273 GATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAA 1332
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAA 240

 Qy 1333 AAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAA 1392
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 Db 241 AAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAA 300

 Qy 1393 CAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACATAAA 1452

Db	301	 CAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACATAAAA	360
Qy	1453	AAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTT	1512
Db	361	 AAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTT	420
Qy	1513	GTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAG	1572
Db	421	 GTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAG	480
Qy	1573	GAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGAT	1632
Db	481	 GAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGAT	540
Qy	1633	TCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTT	1692
Db	541	 TCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTT	600
Qy	1693	GACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGA	1752
Db	601	 GACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGA	660
Qy	1753	ATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATA	1812
Db	661	 ATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATA	720
Qy	1813	GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATAC	1872
Db	721	 GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATAC	780
Qy	1873	CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	1932
Db	781	 CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	840
Qy	1933	GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	1992
Db	841	 GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	900
Qy	1993	ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAAGCTAGAAAGTGCCCTC	2052
Db	901	 ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAAGCTAGAAAGTGCCCTC	960
Qy	2053	CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	2112
Db	961	 CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	1020
Qy	2113	GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	2172
Db	1021	 GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	1080
Qy	2173	GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	2232
Db	1081	 GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	1140
Qy	2233	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAG	2292
Db	1141	 GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAG	1200
Qy	2293	GAGCAAGAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAAGGATGACAATAATCTG	2352

Db	1201	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGACAATAATCTG	1260
Qy	2353	TTAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	2412
Db	1261	TTAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	1320
Qy	2413	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAACGAAATTAGGAACT	2472
Db	1321	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAACGAAATTAGGAACT	1380
Qy	2473	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAG	2532
Db	1381	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAG	1440
Qy	2533	AAACAATTCAAGTGAATTTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGA	2592
Db	1441	AAACAATTCAAGTGAATTTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGA	1500
Qy	2593	GAGAGAAAACCTCAAGAAGAAATGGCTCTGCAGCAAGAGAAAACGGCAACTGGACAAGAA	2652
Db	1501	GAGAGAAAACCTCAAGAAGAAATGGCTCTGCAGCAAGAGAAAACGGCAACTGGACAAGAA	1560
Qy	2653	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	2712
Db	1561	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	1620
Qy	2713	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	2772
Db	1621	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	1680
Qy	2773	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCTGATGAAGAGAAG	2832
Db	1681	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCTGATGAAGAGAAG	1740
Qy	2833	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	2892
Db	1741	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	1800
Qy	2893	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCC	2952
Db	1801	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCC	1860
Qy	2953	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	3012
Db	1861	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	1920
Qy	3013	CATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	3072
Db	1921	CATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	1980
Qy	3073	TTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAA	3132
Db	1981	TTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAA	2040
Qy	3133	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	3192
Db	2041	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	2100
Qy	3193	GGTGTAGGTACTGGAGCAAACCTACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	3252
Db	2101	GGTGTAGGTACTGGAGCAAACCTACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	2160

Qy	3253	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	3312
Db	2161	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	2220
Qy	3313	AACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCT	3372
Db	2221	AACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCT	2280
Qy	3373	TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC	3432
Db	2281	TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC	2340
Qy	3433	TTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGAC	3492
Db	2341	TTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGAC	2400
Qy	3493	TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAG	3552
Db	2401	TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAG	2460
Qy	3553	CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC	3612
Db	2461	CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC	2520
Qy	3613	ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT	3672
Db	2521	ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT	2580
Qy	3673	CAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATAC	3732
Db	2581	CAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATAC	2640
Qy	3733	ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA	3792
Db	2641	ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA	2700
Qy	3793	CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGC	3852
Db	2701	CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGC	2760
Qy	3853	CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCACTTCTCCATCCCC	3912
Db	2761	CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCACTTCTCCATCCCC	2820
Qy	3913	TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAA	3972
Db	2821	TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGTAAGTGGA	2880

RESULT 13

ADB61898

ID ADB61898 standard; cDNA; 2631 BP.

XX

AC ADB61898;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human cDNA encoding clone ASTR020090680.

XX

KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;

KW tissue regeneration; cell regeneration; membrane protein;
 KW signal transduction-related protein; transcription-related protein;
 KW osteoporosis; neurological disease; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1221..2631
 FT /*tag= a
 FT /partial
 FT /product= "Clone ASTR020090680 protein"
 XX
 PN EP1308459-A2.
 XX
 PD 07-MAY-2003.
 XX
 PF 28-MAR-2002; 2002EP-00007401.
 XX
 PR 05-NOV-2001; 2001JP-00379298.
 PR 25-JAN-2002; 2002US-00350978.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-450961/43.
 DR P-PSDB; ADB63868.
 XX
 PT New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 PS Claim 1; Page; 222pp; English.
 XX
 CC The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence
 CC data for this patent is not represented in the printed specification, but
 CC is based on sequence information supplied by the European Patent Office.
 XX

SO Sequence 2631 BP; 875 A; 546 C; 676 G; 534 T; 0 U; 0 Other;

Query Match 34.4%; Score 2403.2; DB 10; Length 2631;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2446; Conservative 0; Mismatches 8; Indels 28; Gaps 1;

Qy	1649	ATTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC	1708
Db	150	AGTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC	209
Qy	1709	AGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGG	1768
Db	210	AGTACCAACAACCTTGAAAGTCGTTTGGAGGAGATACTTTCTAGAATTGCTAAGGAAACGG	269
Qy	1769	AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC	1828
Db	270	AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC	329
Qy	1829	TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG	1888
Db	330	TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG	389
Qy	1889	GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT	1948
Db	390	GCCAGGCAACTCAGGCCCAGAATGAGTGCGGGAAGCTGCGGGATGAGAAAGAGACATTGT	449
Qy	1949	TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG	2008
Db	450	TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG	509
Qy	2009	CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG	2068
Db	510	CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG	569
Qy	2069	TGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGG	2128
Db	570	TGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGG	629
Qy	2129	CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA	2188
Db	630	CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA	689
Qy	2189	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	2248
Db	690	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	749
Qy	2249	CCCTCAAGAATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG	2308
Db	750	CCCTCAAGAATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG	809
Qy	2309	AGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTTAAACAGCAACTTA	2368
Db	810	AGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTTAAACAGCAACTTA	869
Qy	2369	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	2428
Db	870	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	929
Qy	2429	CAGCTCGTGTGGATGAGCTAAGAAGAAAACCTGAAATTAGGAACTGGGGAAATGAACATCC	2488
Db	930	CAGCTCGTGTGGATGAGCTAAGAAGAAAACCTGAAATTAGGAACTGGGGAAATGAACATCC	989

Qy	2489	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	2548
Db	990	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTGCAGAAACAATTCAGTGAAA	1049
Qy	2549	TTCTTGCACGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAACCTCCAAG	2608
Db	1050	TTCTTGCACGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAACCTCCAAG	1109
Qy	2609	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTTCAGGCAGGCCCT	2668
Db	1110	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTTCAGGCAGGCCCT	1169
Qy	2669	GTGAGAGAGCCCTGGAAGCAAGA-----ATGAATTTT	2700
Db	1170	GTGAGAGAGCCCTGGAAGCAAGAGTAAGACAAGGGCAAGAGGCACCTGGAGATGAATTTT	1229
Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACTATTTGCAA	2760
Db	1230	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACTATTTGCAA	1289
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCT	2820
Db	1290	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCT	1349
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Db	1350	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	1409
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
Db	1410	GAAGATGCCAAATCTCAGGGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	1469
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Db	1470	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	1529
Qy	3001	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	1530	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	1589
Qy	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Db	1590	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	1649
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Db	1650	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	1709
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3240
Db	1710	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	1769
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3300
Db	1770	AATGAGACAATGGAACGACAAAGGACAGAGTTGCAAGGCTGCAGAATGTACTAGACCTC	1829
Qy	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3360
Db	1830	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	1889

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Qy      3361 CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAAGACGA 3420
      || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1890 CGCGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAAGACGA 1949

Qy      3421 GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAG 3480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1950 GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAG 2009

Qy      3481 GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA 3540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2010 GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA 2069

Qy      3541 CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG 3600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2070 CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG 2129

Qy      3601 GTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT 3660
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2130 GTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT 2189

Qy      3661 GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTGTGCGCT 3720
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2190 GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTGTGCGCT 2249

Qy      3721 CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATG 3780
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2250 CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATG 2309

Qy      3781 GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT 3840
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2310 ACCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT 2369

Qy      3841 GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC 3900
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2370 GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC 2429

Qy      3901 TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC 3960
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2430 TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC 2489

Qy      3961 TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG 4020
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2490 TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG 2549

Qy      4021 GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT 4080
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2550 GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT 2609

Qy      4081 CATAATATTGATGATCTTTTGC 4102
      |||||||||||||||||||
Db      2610 CATAATATTGATGATCTTTTGC 2631
```

RESULT 14

AAS59821

ID AAS59821 standard; cDNA; 1888 BP.

XX

AC AAS59821;

XX

DT 16-JAN-2002 (first entry)

XX

DE Human novel cytokine encoding cDNA 790CIP2B_6 #1.
 XX
 KW Human; ss; cytokine; cell proliferation; cell differentiation;
 KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;
 KW nervous system disease; neuropathy; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; spinal cord disorder;
 KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
 KW platelet disorder; thrombocytopaenia; stem cell disorder;
 KW aplastic anaemia; tissue regeneration; wound healing; ulcer;
 KW osteoporosis; osteoarthritis; bone degenerative disorder;
 KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;
 KW severe combined immunodeficiency; infection; autoimmune disorder;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;
 KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;
 KW inflammatory bowel disease; food supplement.
 XX
 OS Homo sapiens.
 XX
 PN WO200175093-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US010484.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PR 22-SEP-2000; 2000US-00668680.
 PR 23-OCT-2000; 2000US-00695618.
 PR 30-NOV-2000; 2000US-00728711.
 PR 14-MAR-2001; 2001US-00808701.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;
 PI Drmanac RT;
 XX
 DR WPI; 2001-626432/72.
 DR P-PSDB; AAU68529.
 XX
 PT New polypeptides and nucleic acids, useful for diagnosis, treatment of
 PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
 PT degenerative disorders, cancer and promoting wound healing.
 XX
 PS Claim 1; Page 157-159; 336pp; English.
 XX
 CC The invention relates to isolated human polypeptides (which may be
 CC cytokines) and the polynucleotides encoding them. The protein is useful
 CC for identifying a compound which binds to it (e.g. modulators, agonists
 CC and antagonists). The polynucleotides are useful as an array for mismatch
 CC detection. The proteins and nucleic acids are useful as nutritional
 CC sources or supplements. The protein exhibits activity relating
 CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity, immune stimulating or immune
 CC suppressing and activin or inhibin related activities. The proteins (and
 CC antibodies raised against them) and nucleic acids are therefore useful in
 CC the diagnosis and treatment of diseases and disorders such as cancer,
 CC central and peripheral nervous system diseases and neuropathies,
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
 CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,

thrombocytopaenia, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence encodes a novel protein of the invention

XX

Sequence 1888 BP; 646 A; 409 C; 407 G; 426 T; 0 U; 0 Other;

Query Match 19.1%; Score 1332.8; DB 4; Length 1888;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC	60
Db	450	ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC	509
Qy	61	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTGATTGGA	120
Db	510	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTGATTGGA	569
Qy	121	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	180
Db	570	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	629
Qy	181	GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT	240
Db	630	GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT	689
Qy	241	AGATATATTACAGAGGCCCTCATTAAAAAACTTACTAAACAGGATAATTTGGCTTTGATA	300
Db	690	AGATATATTACAGAGGCCCTCATTAAAAAACTTACTAAACAGGATAATTTGGCTTTGATA	749
Qy	301	AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	360
Db	750	AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	809
Qy	361	TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	420
Db	810	TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	869
Qy	421	GAAAAGTTGGACAAGCTGTTAAAAATTACGTGAACTCAACTTATCATATAACAAAAATCAGC	480
Db	870	GAAAAGTTGGACAAGCTGTTAAAAATTACGTGAACTCAACTTATCATATAACAAAAATCAGC	929
Qy	481	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	540
Db	930	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	989
Qy	541	ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	600
Db	990	ATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	1049

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Qy      601 AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACCGCTTCAAGATTTG 660
      |||
Db      1050 AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACTGCTTCAAGATTTG 1109

Qy      661 ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC 720
      |||
Db      1110 ATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCTTCCTCATTACCTCCAGTTTACC 1169

Qy      721 ATTTTCCACCTCCGTTTCATTGGAAAGTTTGAAGGTCAGCCAGTAACCACTCAGGATAGA 780
      |||
Db      1170 ATTTTCCACCTCCGTTTCATTGGAAAGTTTGAAGGTCAGCCAGTAACCACTCAGGATAGA 1229

Qy      781 CAGGAGGCTTTTGAGAGATTGAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA 840
      |||
Db      1230 CAGGAGGCTTTTGAGAGATTGAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGACCTAGAA 1289

Qy      841 AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTCCCTTGAGGAAATT 900
      |||
Db      1290 AAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTTCCCTTGAGGAAATT 1349

Qy      901 AAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC 960
      |||
Db      1350 AAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAACAGAGC 1409

Qy      961 TGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA 1020
      |||
Db      1410 TGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAGACCATA 1469

Qy      1021 GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA 1080
      |||
Db      1470 GAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTTTATAAA 1529

Qy      1081 ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA 1140
      |||
Db      1530 ATTGATGCTAAATTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAA 1589

Qy      1141 GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA 1200
      |||
Db      1590 GCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACA 1649

Qy      1201 GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA 1260
      |||
Db      1650 GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA 1709

Qy      1261 CAACTTAGAAATGATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAA 1320
      |||
Db      1710 CAACTTAGAAATGATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAA 1769

Qy      1321 GACAAAGAAAAAAAAA 1336
      |||
Db      1770 GACAAAAAAAAAAAAA 1785

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RESULT 15

AED08152

ID AED08152 standard; cDNA; 1888 BP.

XX

AC AED08152;

XX

DT 17-NOV-2005 (first entry)

XX

DE Human CP140 partial cDNA.
 XX
 KW Immune stimulation; gene therapy; drug screening; transgenic animal;
 KW food; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; immune disorder; autonomic nervous system disease;
 KW cns-gen.; neurological disease; central nervous system disease; leukemia;
 KW cytostatic; hematological disease; neoplasm; gene; ss; CP140 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 450..1841
 FT /*tag= a
 FT /product= "Human CP140 protein"
 XX
 PN US2005202422-A1.
 XX
 PD 15-SEP-2005.
 XX
 PF 08-NOV-2002; 2002US-00291128.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 30-MAR-2001; 2001WO-US010484.
 XX
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (CHEN/) CHEN R.
 PA (RENF/) REN F.
 PA (WANG/) WANG D.
 PA (WANG/) WANG J.
 PA (XUCC/) XU C.
 PA (XUEA/) XUE A J.
 PA (YANG/) YANG Y.
 PA (ZHAN/) ZHANG J.
 PA (ZHAO/) ZHAO Q A.
 PA (ZHOU/) ZHOU P.
 PA (GOOD/) GOODRICH R W.
 PA (DRMA/) DRMANAC R T.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ren F, Wang D, Wang J, Xu C;
 PI Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich RW, Drmanac RT;
 XX
 DR WPI; 2005-618089/63.
 DR P-PSDB; AED08195.
 XX
 PT New isolated polynucleotides, useful for treating, preventing, or
 PT ameliorating, e.g. Alzheimer's disease, Parkinson's disease, Huntington's
 PT disease, amyotrophic lateral sclerosis, or leukemia.
 XX
 PS Claim 1; SEQ ID NO 16; 60pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides capable of
 CC inducing an immune response. The polynucleotides and proteins are useful
 CC for treating, preventing or ameliorating a medical condition, e.g.
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, Shy-Drager syndrome or stroke. The
 CC proteins can be used for treating leukemia, inflammatory disorders and
 CC autoimmune disorders, e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes, myasthenia gravis or autoimmune inflammatory eye disease. They
 CC can also be used as nutritional sources and supplements, e.g. as a carbon

CC source, nitrogen source or carbohydrate source. The sequences of the
CC invention are also useful in gene therapy, drug screening and in
CC production of transgenic animals. The present sequence is the human CP140
CC partial cDNA of the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20050202422.

SQ Sequence 1888 BP; 646 A; 409 C; 407 G; 426 T; 0 U; 0 Other;

Query Match 19.1%; Score 1332.8; DB 14; Length 1888;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC	60
Db	450	ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC	509
Qy	61	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTACCTTTGATTGGA	120
Db	510	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTACCTTTGATTGGA	569
Qy	121	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	180
Db	570	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	629
Qy	181	GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT	240
Db	630	GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT	689
Qy	241	AGATATATTACAGAGGCCCTCATTAAAAAACTTACTAAACAGGATAATTTGGCTTTGATA	300
Db	690	AGATATATTACAGAGGCCCTCATTAAAAAACTTACTAAACAGGATAATTTGGCTTTGATA	749
Qy	301	AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	360
Db	750	AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT	809
Qy	361	TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	420
Db	810	TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT	869
Qy	421	GAAAAGTTGGACAAGCTGTTAAAATTACGTGAACTCAACTTATCATATAACAAAATCAGC	480
Db	870	GAAAAGTTGGACAAGCTGTTAAAATTACGTGAACTCAACTTATCATATAACAAAATCAGC	929
Qy	481	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	540
Db	930	AAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAAGCTTAACCTTGCAGGAAATGAA	989
Qy	541	ATTGAGCATATTCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	600
Db	990	ATTGAGCATATTCAGTATGGTTAGGGAAGAAGTTAAAATCTTTGCGAGTCCTCAATTTG	1049
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Db	1050	AAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAAGTTGAAACTGCCTTCAAGATTTG	1109
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Qy	1201	GAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAA	1260
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 01:43:29 ; Search time 1160 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3013.4	43.2	3881	3	US-09-949-016-3905	Sequence 3905, Ap
2	3008.6	43.1	3893	3	US-09-949-016-908	Sequence 908, App
3	2403.2	34.4	2631	3	US-10-104-047-52	Sequence 52, Appl
4	427.8	6.1	499	3	US-09-854-133-333	Sequence 333, App
5	373.4	5.4	375	2	US-08-743-200-11	Sequence 11, Appl
6	323.4	4.6	442	3	US-09-513-999C-2604	Sequence 2604, Ap
7	318.6	4.6	29574	3	US-09-949-016-12650	Sequence 12650, A
8	318.6	4.6	29574	3	US-09-949-016-15647	Sequence 15647, A
9	315	4.5	315	2	US-08-743-200-1	Sequence 1, Appli
10	314.6	4.5	330	2	US-08-743-200-5	Sequence 5, Appli
11	302.6	4.3	784	4	US-09-297-648-2944	Sequence 2944, Ap
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ALIGNMENTS

RESULT 1

US-09-949-016-3905

; Sequence 3905, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE:  CL001307
; CURRENT APPLICATION NUMBER:  US/09/949,016
; CURRENT FILING DATE:  2000-04-14
; PRIOR APPLICATION NUMBER:  60/241,755
; PRIOR FILING DATE:  2000-10-20
; PRIOR APPLICATION NUMBER:  60/237,768
; PRIOR FILING DATE:  2000-10-03
; PRIOR APPLICATION NUMBER:  60/231,498
; PRIOR FILING DATE:  2000-09-08
; NUMBER OF SEQ ID NOS:  207012
; SOFTWARE:  FastSEQ for Windows Version 4.0
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; LENGTH:  3881
; TYPE:  DNA
; ORGANISM:  Human
US-09-949-016-3905

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Best Local Similarity 99.9%;  Pred. No. 0;
Matches 3014;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy	4804	CAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCCAAAA	4863
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US-09-949-016-908

; Sequence 908, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 908
 ; LENGTH: 3893
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-908

Query Match 43.1%; Score 3008.6; DB 3; Length 3893;
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 Matches 3011; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db	503	GAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCATCAT	562
Qy	4084	AATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACAT	4143
Db	563	AATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTACAT	622
Qy	4144	AGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGTCTT	4203
Db	623	AGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGTCTT	682
Qy	4204	ATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAAATT	4263
Db	683	ATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAAATT	742
Qy	4264	GAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTC	4323
Db	743	GAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTC	802
Qy	4324	CTGGCAGAGGCTGAGAGTGAACTTTCATGCACTAAAGAAAAGACAAAAATGCTGTTGAA	4383
Db	803	CTGGCAGAGGCTGAGAGTGAACTTTCATGCACTAAAGAAAAGACAAAAATGCTGTTGAA	862
Qy	4384	AAGTTCACCTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTAGAA	4443
Db	863	AAGTTCACCTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTAGAA	922
Qy	4444	AGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTC	4503
Db	923	AGGAGAGCTCAGGAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTC	982
Qy	4504	CAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAA	4563
Db	983	CAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAA	1042
Qy	4564	ATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAAGGAA	4623
Db	1043	ATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAAGGAA	1102
Qy	4624	AAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAG	4683
Db	1103	AAACTGACAGAAGAGCTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAG	1162
Qy	4684	GATCACCACTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAG	4743

Db	1163	 GATCACCACCTGCAGGTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAG	1222
Qy	4744	CTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGG	4803
Db	1223	 CTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGG	1282
Qy	4804	CAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAA	4863
Db	1283	 CAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAA	1342
Qy	4864	GCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAAGTGAAGTGCAATCAC	4923
Db	1343	 GCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAAGTGAAGTGCAATCAC	1402
Qy	4924	ATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTT	4983
Db	1403	 ATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTT	1462
Qy	4984	CAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAA	5043
Db	1463	 CAGATTAGTGAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAA	1522
Qy	5044	GAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAATATT	5103
Db	1523	 GAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTACAGAATATT	1582
Qy	5104	CTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGACCAA	5163
Db	1583	 CTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGACCAA	1642
Qy	5164	AGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAG	5223
Db	1643	 AGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAACTGGAGTTAGAG	1702
Qy	5224	AATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTT	5283
Db	1703	 AATTTGCAGCAGATATCCCAGCAGCAGAAAGGGGAAATAGAGTGGCAGAAGCAGCTCCTT	1762
Qy	5284	GAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCGTGT	5343
Db	1763	 GAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCTTTACAATCGTGT	1822
Qy	5344	GTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAAAAA	5403
Db	1823	 GTTGAGTGTTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGACATTTGGGAAAAA	1882
Qy	5404	AAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAA	5463
Db	1883	 AAGTTGGCACAAACCAAAAGGGTTTTAGCAGCAGCAGAAGAAAATAGCAAAATGGAGCAA	1942
Qy	5464	TCAAACCTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAACCTAGACCAACTA	5523
Db	1943	 TCAAACCTAGAAAAGTTGGAATTGAATGTCAGAAAACCTGCAGCAGGAACCTAGACCAACTA	2002
Qy	5524	AACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAA	5583
Db	2003	 AACAGAGACAAGTTGTCACTGCATAACGACATTTTCAGCAATGCAACAGCAGCTCCAAGAA	2062
Qy	5584	AAACGAGAAGCAGTAAACTCACTGCAGGAGGAAGTAACTGCTAATGTCCAAGACCATTTGAAC	5643

Db	2063	AAACGAGAAGCAGTAAACTCACTGCAGGAGGAACTAGCTAATGTCCAAGACCATTGTAAC	2122
Qy	5644	CTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAG	5703
Db	2123	CTAGCAAAACAGGACCTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAG	2182
Qy	5704	ACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAAGAA	5763
Db	2183	ACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTTGAAGACTGTCAGAAAGAA	2242
Qy	5764	GAGGAGACAAAACAACAACAACTTCAAGTGCTTCAGAATGAGATTGAAGAAAAACAAGCTC	5823
Db	2243	GAGGAGACAAAACAACAACAACTTCAAGTGCTTCAGAATGAGATTGAAGAAAAACAAGCTC	2302
Qy	5824	AAACTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAA	5883
Db	2303	AAACTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAA	2362
Qy	5884	AGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAA	5943
Db	2363	AGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAA	2422
Qy	5944	TTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAG	6003
Db	2423	TTAACAGACCAGAAAAGCAAACCTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAG	2482
Qy	6004	CGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCC	6063
Db	2483	CGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCC	2542
Qy	6064	CAAACCTAAACGGCAGCTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTG	6123
Db	2543	CAAACCTAAACGGCAGCTTTCAGAAAGGGAGCAGCAATTGGTGGAGAAATCAGGTGAGCTG	2602
Qy	6124	TTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAG	6183
Db	2603	TTGGCCCTCCAGAAAGAGGCAGATTCTATGAGGGCAGACTTCAGCCTTCTGCGGAACCAG	2662
Qy	6184	TTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAG	6243
Db	2663	TTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAGGAAGCACTTAAG	2722
Qy	6244	ATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATA	6303
Db	2723	ATCCAGCGGAGCCAGCTGGAGAAAAACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATA	2782
Qy	6304	CAAAGGAAATGGCAACAATTGAACTGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGC	6363
Db	2783	CAAAGGAAATGGCAACAATTGAACTGGTAGCCCAGGACAACCATGAGCGGGCCAGGCGC	2842
Qy	6364	CTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATGGCA	6423
Db	2843	CTGATGAAGGAGCTCAACCAGATGCAGTATGAGTACACGGAGCTCAAGAAACAGATGGCA	2902
Qy	6424	AACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTTAAA	6483
Db	2903	AACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATGAGGACACTTAAA	2962
Qy	6484	TCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAA	6543
Db	2963	TCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCAGAA	3022

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Qy      6544 CTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAA 6603
          |||
Db      3023 CTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAAGGAGAATTGGAA 3082

Qy      6604 AGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTGAAC 6663
          |||
Db      3083 AGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAAGAAAACTGAAC 3142

Qy      6664 TTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAACTG 6723
          |||
Db      3143 TTTTCCCAAGTTCACATAATGGATGAACACTGGCGTGGAGAAGCACTCCGGGAGAACTG 3202

Qy      6724 CGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCAGAA 6783
          |||
Db      3203 CGTCACCGGGAAGACCGACTCAAGGCCCAACTCCGACACTGTATGTCCAAGCAAGCAGAA 3262

Qy      6784 GTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTA 6843
          |||
Db      3263 GTATTAATTAAAGGAAAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTA 3322

Qy      6844 GATGCTTTAGGGGAATTGGTCAACAGCACCTCTGCAGATTTCAGCGTCATCACCCAGTCTG 6903
          |||
Db      3323 GATGCTTTAGGGGAATTGGTCAACAGCACCTCTGCAGATTTCAGCGTCATCACCCAGTCTG 3382

Qy      6904 TCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAGAAT 6963
          |||
Db      3383 TCTCAGCTGGAGTCTTCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAGAAT 3442

Qy      6964 GCCTCAGCCAGATGA 6978
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Db      3443 GCCTCAGCCAGATGA 3457

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RESULT 3

US-10-104-047-52

; Sequence 52, Application US/10104047

; Patent No. 6943241

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 6943241el full length cDNA

; FILE REFERENCE: H1-A0105

; CURRENT APPLICATION NUMBER: US/10/104,047

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 52

; LENGTH: 2631

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-104-047-52

Query Match 34.4%; Score 2403.2; DB 3; Length 2631;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 2446; Conservative 0; Mismatches 8; Indels 28; Gaps 1;

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Qy      1649 ATCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC 1708
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Db      150 AGTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC 209

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Qy	1709	AGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGG	1768
Db	210	AGTACCAACAACCTTGAAAGTCGTTTGGAGGAGATACTTTCTAGAATTGCTAAGGAAACGG	269
Qy	1769	AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC	1828
Db	270	AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC	329
Qy	1829	TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG	1888
Db	330	TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG	389
Qy	1889	GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT	1948
Db	390	GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT	449
Qy	1949	TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG	2008
Db	450	TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG	509
Qy	2009	CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG	2068
Db	510	CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG	569
Qy	2069	TGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGG	2128
Db	570	TGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGG	629
Qy	2129	CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA	2188
Db	630	CTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAA	689
Qy	2189	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	2248
Db	690	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	749
Qy	2249	CCCTCAAGAATGCCCTTGAAAAAGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG	2308
Db	750	CCCTCAAGAATGCCCTTGAAAAAGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTG	809
Qy	2309	AGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAAACAGCAACTTA	2368
Db	810	AGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTAAAAACAGCAACTTA	869
Qy	2369	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	2428
Db	870	AAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCAGAAGAAGTGG	929
Qy	2429	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAAGTGGGAAATGAACATCC	2488
Db	930	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAAGTGGGAAATGAACATCC	989
Qy	2489	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	2548
Db	990	ATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAA	1049
Qy	2549	TTCTTGCACGCTCCAAGTGGGAAAAGAGATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAG	2608
Db	1050	TTCTTGCACGCTCCAAGTGGGAAAAGAGATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAG	1109

Qy	2609	AAGAAATGGCTCTGCAGCAAGAGAACTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCT	2668
Db	1110	AAGAAATGGCTCTGCAGCAAGAGAACTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCT	1169
Qy	2669	GTGAGAGAGCCCTGGAAGCAAGA-----ATGAATTTT	2700
Db	1170	GTGAGAGAGCCCTGGAAGCAAGAGTAAGACAAGGGCAAGAGGCACCTGGAGATGAATTTT	1229
Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACTATTTGCAA	2760
Db	1230	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACTATTTGCAA	1289
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACTTCAGGAAGCT	2820
Db	1290	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACTTCAGGAAGCT	1349
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Db	1350	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	1409
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
Db	1410	GAAGATGCCAAATCTCAGGGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	1469
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Db	1470	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	1529
Qy	3001	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	1530	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	1589
Qy	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Db	1590	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAA	1649
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Db	1650	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	1709
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3240
Db	1710	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	1769
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTC	3300
Db	1770	AATGAGACAATGGAACGACAAAGGACAGAGTTGCAAGGCTGCAGAATGTACTAGACCTC	1829
Qy	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3360
Db	1830	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	1889
Qy	3361	CGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAAGACGA	3420
Db	1890	CGCGAAGTTTCTTATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAAGACGA	1949
Qy	3421	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	3480
Db	1950	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	2009
Qy	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3540

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      |||
Db      2010 GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA 2069
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Qy      3541 CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG 3600
      |||
Db      2070 CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG 2129
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Qy      3601 GTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT 3660
      |||
Db      2130 GTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT 2189
      |||
Qy      3661 GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCT 3720
      |||
Db      2190 GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCT 2249
      |||
Qy      3721 CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATG 3780
      |||
Db      2250 CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATG 2309
      |||
Qy      3781 GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT 3840
      |||
Db      2310 ACCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT 2369
      |||
Qy      3841 GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC 3900
      |||
Db      2370 GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC 2429
      |||
Qy      3901 TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCTGAACACCATAAC 3960
      |||
Db      2430 TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCTGAACACCATAAC 2489
      |||
Qy      3961 TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG 4020
      |||
Db      2490 TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG 2549
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Qy      4021 GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT 4080
      |||
Db      2550 GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT 2609
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Qy      4081 CATAATATTGATGATCTTTTGC 4102
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Db      2610 CATAATATTGATGATCTTTTGC 2631

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RESULT 4

US-09-854-133-333

; Sequence 333, Application US/09854133

; Patent No. 6759508

; GENERAL INFORMATION:

; APPLICANT: Lodes, Michael J.

; APPLICANT: Mohamath, Raodoh

; APPLICANT: Henderson, Robert A.

; APPLICANT: Benson, Darin R.

; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.475C10

; CURRENT APPLICATION NUMBER: US/09/854,133

; CURRENT FILING DATE: 2001-05-11

; NUMBER OF SEQ ID NOS: 735

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 333
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-333

Query Match 6.1%; Score 427.8; DB 3; Length 499;
Best Local Similarity 99.5%; Pred. No. 1.4e-93;
Matches 429; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC 60
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Db      69 ATGAAGAAAGGTTCTCAACAAAAAATATTCTCCAAAGCAAAGATACCATCATCATCTCAC 128

Qy     61 TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTCACCTTTGATTGGA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACCTTTCACCTTTGATTGGA 188

Qy    121 TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAAGTTGAGATTGCAGAT 248

Qy    181 GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 GAAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTCACATGCAGGAGTT 308

Qy    241 AGATATATTACAGAGGCCCTCATTAAAAAAATTACTAAACAGGATAATTTGGCTTTGATA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 AGATATATTACAGAGGCCCTCATTAAAAAAATTACTAAACAGGATAATTTGGCTTTGATA 368

Qy    301 AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 AAATCTCTGAACCTTTCACTTTCTAAAGACGGTGGCAAGAAATTTAAGTATATTGAGAAT 428

Qy    361 TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 TTGGAAAAATGTGTTAAACTTGAAGTACTGAATCTCAGCTATAATCTAATAGGGAAGATT 488

Qy    421 GAAAAGTTGGA 431
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Db    489 GAAAAGTCGGA 499
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RESULT 5

US-08-743-200-11

; Sequence 11, Application US/08743200
; Patent No. 5861260
; GENERAL INFORMATION:
; APPLICANT: Doxsey, Stephen J.
; TITLE OF INVENTION: DIAGNOSTIC METHODS FOR SCREENING
; TITLE OF INVENTION: PATIENTS FOR SCLERODERMA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/743,200
;   FILING DATE:  05-NOV-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Fasse, J. Peter
;   REGISTRATION NUMBER:  32,983
;   REFERENCE/DOCKET NUMBER:  07917/025001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  617-542-5070
;   TELEFAX:  617-542-8906
;   INFORMATION FOR SEQ ID NO:  11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  375 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;   NAME/KEY:  Coding Sequence
;   LOCATION:  2...373
US-08-743-200-11

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Query Match          5.4%;  Score 373.4;  DB 2;  Length 375;
Best Local Similarity 99.7%;  Pred. No. 1.9e-80;
Matches 374;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      2043 AAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCT 2102
          |||
Db      1 AAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCT 60

Qy      2103 CAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCA 2162
          |||
Db      61 CAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCA 120

Qy      2163 GCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCA 2222
          |||
Db      121 GCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCA 180

Qy      2223 AGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGGCCAGTTCTC 2282
          |||
Db      181 AGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGGCCAGTTCTC 240

Qy      2283 AGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGA 2342
          |||
Db      241 AGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGA 300

Qy      2343 CAATAATCTGTTAAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGA 2402
          |||
Db      301 CAATAATCTGTTAAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGA 360

Qy      2403 TGGTTTGGTTCGTCC 2417
          |||
Db      361 TGGTTTGGTTCGTCC 375

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RESULT 6

US-09-513-999C-2604

; Sequence 2604, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

: APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

```
; NUMBER OF SEQ ID NOS: 36681
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; SOFTWARE: Patent.pm

; SEO ID NO 2604

; LENGTH: 442

; TYPE: DNA

; ORGANISM: Homo sapiens

: FEATURE:

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; NAME/KEY: CDS
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; LOCATION: 126..440

FEATURE:

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; NAME/KEY: misc feature
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; LOCATION: 32

OTHER INFORMATION: k=q or t

US-09-513-999C-2604

Query Match 4.6%; Score 323.4; DB 3; Length 442;

Best Local Similarity 99.7%; Pred. No. 2.7e-68;

Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1649 ATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC 1708

Db 118 AGTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC 177

Qy 1709 AGTACCAACAAGTTGAAAGTCGTTTGATGAGATACTTTCTAGAATTGCTAAGGAAAACGG 1768
 | | | | | | | | | | | | | | | | | | | | | | | |

Db 178 AGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGG 237

QY 1769 AAGAGATTAAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC 1828

Db 238 AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC 297

Qy 1829 TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG 1888

Db 298 TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAG 357

Qy 1889 GCCAGGCAACTCAGGCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT 1948

Db 358 GCCAGGCAACTCAGGCCAGGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT 417

Qy 1949 TGCAGAGATTGACAGAAGTCGAGCA 1973
 |||||

Db 418 TGCAGAGATTGACAGAAAGTCGAGCA 442

RESULT 7

US-09-949-016-12650

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; Sequence 12650, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12650
; LENGTH: 29574
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12650
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Query Match          4.6%; Score 318.6; DB 3; Length 29574;
Best Local Similarity 98.8%; Pred. No. 3e-66;
Matches 321; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy      3648 AGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACC 3707
          |||
Db      126  AGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACC 185

Qy      3708 CCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGT 3767
          |||
Db      186  CCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGT 245

Qy      3768 ACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCT 3827
          |||
Db      246  ACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCT 305

Qy      3828 CACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCC 3887
          |||
Db      306  CACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCC 365

Qy      3888 TCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCC 3947
          |||
Db      366  TCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCC 425

Qy      3948 TGAACACCATAACTTAGAGAATGAA 3972
          |||
Db      426  TGAACACCATAACTTAGTAAGTGA 450
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RESULT 8

US-09-949-016-15647

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; Sequence 15647, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15647
; LENGTH: 29574
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15647
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Query Match          4.6%; Score 318.6; DB 3; Length 29574;
Best Local Similarity 98.8%; Pred. No. 3e-66;
Matches 321; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
Qy      3648 AGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACC 3707
          |||
Db      126 AGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACC 185

Qy      3708 CCCATTTGTGCCTCCTCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCTCTGT 3767
          |||
Db      186 CCCATTTGTGCCTCCTCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCTCTGT 245

Qy      3768 ACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCT 3827
          |||
Db      246 ACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCT 305

Qy      3828 CACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCC 3887
          |||
Db      306 CACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCC 365

Qy      3888 TCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCC 3947
          |||
Db      366 TCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCC 425

Qy      3948 TGAACACCATAACTTAGAGAATGAA 3972
          |||
Db      426 TGAACACCATAACTTAGTAAGTGGA 450
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RESULT 9

US-08-743-200-1

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; Sequence 1, Application US/08743200
; Patent No. 5861260
; GENERAL INFORMATION:
; APPLICANT: Doxsey, Stephen J.
; TITLE OF INVENTION: DIAGNOSTIC METHODS FOR SCREENING
; TITLE OF INVENTION: PATIENTS FOR SCLERODERMA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,200
; FILING DATE: 05-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07917/025001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...315
US-08-743-200-1

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Query Match          4.5%; Score 315; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.5e-66;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      775 GATAGACAGGAGGCTTTTGAGAGATTGAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGAC 834
        |||
Db      1 GATAGACAGGAGGCTTTTGAGAGATTGAGTTTAGAAGAGGTAGAAAGACTGGAAAGAGAC 60

Qy      835 CTAGAAAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTCCTTGAG 894
        |||
Db      61 CTAGAAAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACAAACAAGGTCCTTGAG 120

Qy      895 GAAATTAAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAA 954
        |||
Db      121 GAAATTAAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGAGGCCATGTTACAGAAA 180

Qy      955 CAGAGCTGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAG 1014
        |||
Db      181 CAGAGCTGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGAATTGCTAAAACAGAAG 240

Qy      1015 ACCATAGAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTT 1074
        |||
Db      241 ACCATAGAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGAACAGGAATTGGCCTTT 300

Qy      1075 TATAAAATTGATGCT 1089
        |||
Db      301 TATAAAATTGATGCT 315

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```

RESULT 10
US-08-743-200-5

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; Sequence 5, Application US/08743200
; Patent No. 5861260
; GENERAL INFORMATION:
;   APPLICANT:  Doxsey, Stephen J.
;   TITLE OF INVENTION:  DIAGNOSTIC METHODS FOR SCREENING
;   TITLE OF INVENTION:  PATIENTS FOR SCLERODERMA
;   NUMBER OF SEQUENCES:  36
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Fish & Richardson P.C.
;     STREET:  225 Franklin Street
;     CITY:  Boston
;     STATE:  MA
;     COUNTRY:  US
;     ZIP:  02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/743,200
;     FILING DATE:  05-NOV-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fasse, J. Peter
;     REGISTRATION NUMBER:  32,983
;     REFERENCE/DOCKET NUMBER:  07917/025001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-542-5070
;     TELEFAX:  617-542-8906
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  330 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  3...329
US-08-743-200-5

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Query Match 4.5%; Score 314.6; DB 2; Length 330;
Best Local Similarity 97.3%; Pred. No. 3.2e-66;
Matches 320; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

[illegible]

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Db      182  |||||ACTTGTAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAA 241
Qy      1569 GCAGGAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCT 1628
Db      242  |||||GCAGGAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCT 301
Qy      1629 GGATTCCAAAGACCCAAAACATTCCCATA 1657
Db      302  |||||GGATTCCAAAGACCCAAAACATTCCCATA 330

```

RESULT 11

US-09-297-648-2944

; Sequence 2944, Application US/09297648

; Patent No. 6964868

; GENERAL INFORMATION:

; APPLICANT: Williams, Lewis T.

; APPLICANT: Escobedo, Jaime

; APPLICANT: Innis, Michael A.

; APPLICANT: Garcia, Pablo Dominiguez

; APPLICANT: Sudduth-Klinger, Julie

; APPLICANT: Reinhard, Christoph

; APPLICANT: Giese, Klaus

; APPLICANT: Randazzo, Filippo

; APPLICANT: Kennedy, Giulia C.

; APPLICANT: Pot, David

; APPLICANT: Kassan, Altaf

; APPLICANT: Lamson, George

; APPLICANT: Drmanac, Radoje

; APPLICANT: Crkvenjakov, Radomir

; APPLICANT: Dickson, Mark

; APPLICANT: Drmanac, Snezana

; APPLICANT: Labat, Ivan

; APPLICANT: Leshkowitz, Dena

; APPLICANT: Kita, David

; APPLICANT: Garcia, Veronica

; APPLICANT: Jones, William Lee

; APPLICANT: Stache-Crain, Birjit

; TITLE OF INVENTION: No. 6964868el Human Genes and Gene Expression

; TITLE OF INVENTION: Products II

; FILE REFERENCE: 2300-1481

; CURRENT APPLICATION NUMBER: US/09/297,648

; CURRENT FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 60/072,910

; PRIOR FILING DATE: 1998-01-28

; PRIOR APPLICATION NUMBER: 60/075,954

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/080,666

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/080,515

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/080,114

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/105,234

; PRIOR FILING DATE: 1998-10-21

; NUMBER OF SEQ ID NOS: 5252

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2944

; LENGTH: 784

; TYPE: DNA

Query Match 4.3%; Score 302.6; DB 4; Length 784;
Best Local Similarity 69.5%; Pred. No. 4e-63;
Matches 453; Conservative 0; Mismatches 187; Indels 12; Gaps 7;

Qy	5680	CAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCA-AA	5738
Db	52	CACGAGGTGTTGCTCAANGAGCAGACCCGACTCCNTAAGGTCATCATTGAATGGGCATNA	111
Qy	5739	TAGGTTTGAAGACTGTCTAGAAAAGAAGAGGAGACAAAACAACAACACTTCAAGTGCTTCA	5798
Db	112	TANGTTTGAANACTGTCCAANANANTANGNGTCAATACATCAACNNCTTTANNTGCTTGA	171
Qy	5799	GAATGAGATTGAAGAAAAACAAGCTCAAAGTCTCAACAAGAAATGATGTTTCAGAGACT	5858
Db	172	TATTGNNTTGAANAACACANGNCTCNGNCTAGTTTCGCCTGANATGATGTTTAAGATACT	231
Qy	5859	CCAGAAAGAGAGAGAAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGA	5918
Db	232	CCGGAAGGAGACANANTGTTNTGANTGCGGATTAGANACCACNGAAGNNACACTNAAGGA	291
Qy	5919	GCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAAGTGGACCAAGTGCT	5978
Db	292	NCANCATCTCCACCTNGNAACTGNATTNNCNGACCANAAAAGNGAACTGGACCAAATGCT	351
Qy	5979	CTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAGGAAGAGGAGAGGTGGTG	6038
Db	352	CTCAAAGGTGCTGGCAGCTTAANAGCGTGTTANGACTCTGCACGAAGANGACAGGTNNTN	411
Qy	6039	TGAGAGCCTGGAGAAGACACTCTCCCAAATAAAACGGCAGCTTT---CAGAAAGGGAGCA	6095
Db	412	TGAGAGCCTGGNNANNACACTCTCCCAAATAAACTGNANCTTTCAACANANGGGANCCC	471
Qy	6096	GCAATTGGTGGAGAAATCAGGTGAGCTGTTGGCCC-TCCAGAAAGAGGCAGATTCTATGA	6154
Db	472	CANNTTGGTGGAGAAATCAGGTGANCTGTTGGCCCTTCCACAAAGANGCAAATTCNTNGA	531
Qy	6155	GGGC-AGACTTCAGCC-TTCTGCGGAACCAAGTTCTTGACAGAAAGAAAGAAAGC---TGA	6209
Db	532	GGGCNAGACTTNANCCTTTTTGTCNGAACCAAGTNCCTTGACTGACTAAATGAAAGCTTTTA	591
Qy	6210	GAAGCAGGTGGCCAGCCTGAAGGAAGCA--CTTAAGATCCAGCGGAGCCAGCTGGAGAAA	6267
Db	592	AGCCAGGTGGCCANCCTTAANGAAGCNACTTTTTAATCCANCGGAACCNGCTTGAGANA	651
Qy	6268	AACCTTCTTGAGCAAAAACAGGAGAACAGCTGCATACAAAAGGAAATGGCAA	6319
Db	652	AAACCNTTTTTGACCCAAAACNCGGAGAACCAGCTGGCCTACCAAAGGGAAA	703

http://es/ScoreAccessWeb/GetItem.action?AppId=10663433&seqId=585793&ItemName=us... 8/25/06

```

; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, William Lee
; APPLICANT: Stache-Crain, Birjit
; TITLE OF INVENTION: No. 6964868el Human Genes and Gene Expression
; TITLE OF INVENTION: Products II
; FILE REFERENCE: 2300-1481
; CURRENT APPLICATION NUMBER: US/09/297,648
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,666
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,515
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 5252
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1518
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-297-648-1518

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```

Query Match          4.3%; Score 300; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      5686 GTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTT 5745
          |||
Db      1 GTGTTGCTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGGTTT 60

Qy      5746 GAAGACTGTCAGAAAGAAGAGGAGACAAACAACAACACTTCAAGTGCTTCAGAATGAG 5805
          |||
Db      61 GAAGACTGTCAGAAAGAAGAGGAGACAAACAACAACACTTCAAGTGCTTCAGAATGAG 120

Qy      5806 ATTGAAGAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAA 5865
          |||

```

```

Db      121 ATTGAAGAAAACAAGCTCAAAGCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAA 180
Qy      5866 GAGAGAGAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAG 5925
        |||
Db      181 GAGAGAGAAAGTGAAGAAAGCAAATTAGAAACCAGTAAAGTGACACTGAAGGAGCAACAG 240
Qy      5926 CACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAAGTGGACCAAGTGCTCTCAAAG 5985
        |||
Db      241 CACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGCAAAGTGGACCAAGTGCTCTCAAAG 300

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RESULT 13

US-08-743-200-13

; Sequence 13, Application US/08743200

; Patent No. 5861260

; GENERAL INFORMATION:

; APPLICANT: Doxsey, Stephen J.

; TITLE OF INVENTION: DIAGNOSTIC METHODS FOR SCREENING

; TITLE OF INVENTION: PATIENTS FOR SCLERODERMA

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743,200

; FILING DATE: 05-NOV-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07917/025001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1...228

US-08-743-200-13

Query Match 3.3%; Score 228; DB 2; Length 228;

Best Local Similarity 100.0%; Pred. No. 2.8e-45;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2575  GATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAA 2634
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Db      121   GATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAA 180

Qy      2635  CTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAGCCCTG 2682
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RESULT 14

US-09-949-016-35518

; Sequence 35518, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 35518

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-35518

Query Match 3.2%; Score 224.4; DB 3; Length 601;

Best Local Similarity 99.6%; Pred. No. 3.3e-44;

Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      376  AAGATGTTTCAGAGACTCCAGAAAGAGAGAGAAAGTGAAGAAAGCAAATTAGAAACCACT 435

Qy      5902  AAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGC 5961
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Db      436  AAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGC 495

Qy      5962  AACTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTAGGACTCTGCAG 6021
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Db      496  AACTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTAGGACTCTGCAG 555

Qy      6022  GAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAA 6067
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RESULT 15

US-09-949-016-138497

; Sequence 138497, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

: PRIOR APPLICATION NUMBER: 60/231,498

: PRIOR FILING DATE: 2000-09-08

: NUMBER OF SEO ID NOS: 207012

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 138497

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-138497

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Best Local Similarity 99.6%; Pred. No. 3.3e-44;

Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Ov 5902 AAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGC 5961

Db 436 AAAGTGACACTGAAGGAGCAACAGCACCAGCTGGAAAAGGAATTAACAGACCAGAAAAGC 495

Qy 5962 AACTGGACCAAGTGCTCTCAAAGGTGCTGGCAGCTGAAGAGCGTGTTAGGACTCTGCAG 6021

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Qy 6022 GAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAA 6067

Db 556 GAAGAGGAGAGGTGGTGTGAGAGCCTGGAGAAGACACTCTCCCAA 601

Search completed: August 15, 2006, 02:02:57

Job time : 1161 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10663433 and Search Result us-10-663-433- 1.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10663433 and Search Result us-10-663-433-1.rge.

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 00:51:02 ; Search time 62234 Seconds
(without alignments)
7170.118 Million cell updates/sec

Title: US-10-663-433-1
Perfect score: 6978
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_pat:*
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- 6: gb_ro:*
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- 8: gb_sy:*
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- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6978	100.0	6978	5	AF513978	AF513978 Homo sapi
2	5350.8	76.7	5804	5	AK074079	AK074079 Homo sapi
3	3735	53.5	3735	5	AY651261	AY651261 Homo sapi
4	3597.4	51.6	3602	2	CQ850900	CQ850900 Sequence
5	3597.4	51.6	3602	5	AK128098	AK128098 Homo sapi
6	3008.6	43.1	3893	5	AF083322	AF083322 Homo sapi
7	3000.8	43.0	3882	2	CQ724459	CQ724459 Sequence
8	2890.2	41.4	3037	5	BC002932	BC002932 Homo sapi
9	2873.6	41.2	3044	2	CS168804	CS168804 Sequence
10	2873.6	41.2	3044	2	AX834925	AX834925 Sequence
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12	2786.8	39.9	2803	5	BC009287	BC009287 Homo sapi
13	2410.4	34.5	3974	6	AK131139	AK131139 Mus muscu
14	2403.2	34.4	2631	2	AR717552	AR717552 Sequence
15	2403.2	34.4	2631	2	AX746527	AX746527 Sequence
16	2403.2	34.4	2631	5	AK090600	AK090600 Homo sapi
17	1826.4	26.2	3008	6	MMIB35	X79131 M.musculus
18	1643.4	23.6	1833	5	AK093457	AK093457 Homo sapi
19	1331	19.1	1600	5	BC089415	BC089415 Homo sapi
20	1213	17.4	2766	6	BC038386	BC038386 Mus muscu
21	1075.2	15.4	1879	6	BC060146	BC060146 Mus muscu
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23	707.2	10.1	791	2	BD079470	BD079470 Cancer-as
24	531.8	7.6	667	2	BD221466	BD221466 Human gen
25	461.4	6.6	514	2	BD058388	BD058388 Secreted
26	427.8	6.1	499	2	AR563069	AR563069 Sequence
27	427.8	6.1	499	2	AX321802	AX321802 Sequence
28	375.2	5.4	1321	11	BX931302	BX931302 Gallus ga
29	373.4	5.4	375	2	AR030354	AR030354 Sequence
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31	323.4	4.6	442	2	AR726612	AR726612 Sequence
32	323.4	4.6	442	2	AX886741	AX886741 Sequence
33	318.6	4.6	147029	5	AL137068	AL137068 Human DNA
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37	302.6	4.3	784	2	BD214802	BD214802 Novel hum
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44	279.2	4.0	669	11	BX933773	BX933773 Gallus ga
45	257.2	3.7	974	11	BX931123	BX931123 Gallus ga

ALIGNMENTS

RESULT 1
AF513978

LOCUS AF513978 6978 bp mRNA linear PRI 24-MAY-2003
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 ACCESSION AF513978
 VERSION AF513978.1 GI:31071794
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 6978)
 AUTHORS Gromley,A., Jurczyk,A., Sillibourne,J., Halilovic,E., Mogensen,M.,
 Groisman,I., Blomberg,M. and Doxsey,S.
 TITLE A novel human protein of the maternal centriole is required for the
 final stages of cytokinesis and entry into S phase
 JOURNAL J. Cell Biol. 161 (3), 535-545 (2003)
 PUBMED 12732615
 REFERENCE 2 (bases 1 to 6978)
 AUTHORS Gromley,A.S., Jurczyk,A., Sillibourne,J.E., Halilovic,E. and
 Doxsey,S.J.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAY-2002) Molecular Medicine, University of
 Massachusetts Medical School, 373 Plantation St., Biotech II,
 Worcester, MA 01605, USA
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 /db_xref="taxon:9606"
 /chromosome="9"
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 /protein_id="AAP43846.1"
 /db_xref="GI:31071795"
 /translation="MKKGSQQKIFSKAKIPSSSSHSPIPSSMSNMRSRSLSPILIGSETL
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ORIGIN

Query Match 100.0%; Score 6978; DB 5; Length 6978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACTTTCACCTTTGATTGGA	120
Db	61	TCTCCTATCCCATCATCTATGTCCAATATGAGATCTAGGTCACTTTCACCTTTGATTGGA	120
Qy	121	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	180
Db	121	TCAGAGACTCTACCTTTTCATTCTGGAGGACAGTGGTGTGAGCAAATTGAGATTGCAGAT	180
Qy	181	GAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTACATGCAGGAGTT	240
Db	181	GAAACAATATGCTTTTGGACTATCAAGACCATAAAGGAGCTGATTACATGCAGGAGTT	240
Qy	241	AGATATATTACAGAGGCCCTCATTAAAAAACTTACTAAACAGGATAATTTGGCTTTGATA	300
Db	241	AGATATATTACAGAGGCCCTCATTAAAAAACTTACTAAACAGGATAATTTGGCTTTGATA	300
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Db	1921	AAGCTGCGGGATGAGAAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGA	1980
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Db	1981	GACCAGCTGGAATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGACAGAGCTA	2040
Qy	2041	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2100
Db	2041	GAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGAT	2100
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Db	2101	CTCAGTGCCATGAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAAC	2160
Qy	2161	CAGCTCAAGGAAGAGTTGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2220
Db	2161	CAGCTCAAGGAAGAGTTGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTT	2220
Qy	2221	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCCAGTTC	2280
Db	2221	CAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCCAGTTC	2280
Qy	2281	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGAT	2340
Db	2281	TCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGAT	2340
Qy	2341	GACAATAATCTGTTAAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2400
Db	2341	GACAATAATCTGTTAAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTT	2400
Qy	2401	GATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTG	2460

Db	2401	GATGGTTTGGTTCGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAACTG	2460
Qy	2461	AAATTAGGAACTGGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2520
Db	2461	AAATTAGGAACTGGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTT	2520
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Db	2521	GCTGATTTACAGAAACAATTCAAGTGAATTCTTGACGCTCCAAGTGGGAAAGAGATGAA	2580
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Qy	2641	ACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTT	2700
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Db	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
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Db	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Qy	3001	CTGAAGTCCCTTCATGGAACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	3001	CTGAAGTCCCTTCATGGAACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Qy	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Db	3061	GAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
Qy	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Db	3121	GCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAG	3180
Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAAACTG	3240
Db	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAAACTG	3240
Qy	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAAATGTACTAGACCTC	3300
Db	3241	AATGAGACAATGGAACGACAAAGGACAGAGATTGCAAGGCTGCAGAAATGTACTAGACCTC	3300
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Db	3301	ACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGA	3360
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Db	3361	CGTGAAGTTTCTTATCAGAAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGA	3420
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Db	3421	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	3480
Qy	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3540
Db	3481	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	3540
Qy	3541	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600
Db	3541	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600
Qy	3601	GTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3660
Db	3601	GTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGT	3660
Qy	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTGTGCCT	3720
Db	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTGTGCCT	3720
Qy	3721	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCAGGGCATG	3780
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Qy	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
Db	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
Qy	3841	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC	3900
Db	3841	GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC	3900
Qy	3901	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3960
Db	3901	TTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAAC	3960
Qy	3961	TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4020
Db	3961	TTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGG	4020
Qy	4021	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4080
Db	4021	GAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAAGAACTGCAT	4080
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Db	4081	CATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTAGAAGAATTA	4140
Qy	4141	CATAGAACTGTCCAGAAACGTCAACAGCAAAAGGACTTCATTGATGGAAATGTTGAGAGT	4200
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Qy	4201	CTTATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATTGTAGATGAA	4260
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Qy	4321	CTCCTGGCAGAGGCTGAGAGTGAACCTTTCATGCACTAAAGAAAAGACAAAAATGCTGTT	4380
Db	4321	CTCCTGGCAGAGGCTGAGAGTGAACCTTTCATGCACTAAAGAAAAGACAAAAATGCTGTT	4380
Qy	4381	GAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTA	4440
Db	4381	GAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAACCTGAGTCAGATGCTGAGGAATTA	4440
Qy	4441	GAAAGGAGAGCTCAGGAAACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCG	4500
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Qy	4861	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAAT	4920
Db	4861	AAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAAT	4920
Qy	4921	CACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	4980
Db	4921	CACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAAT	4980
Qy	4981	G TTCAGATTAGTGAAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAGAG	5040
Db	4981	G TTCAGATTAGTGAAAAGAAAACTCAACTTACACTTATAAAGCAGGAAATTGAAAAGAG	5040
Qy	5041	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5100
Db	5041	GAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAACTAAAGAAT	5100
Qy	5101	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5160
Db	5101	ATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTACAACATGAC	5160

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Db	6481		AAATCTGAGGTGAAGGATGAAATCAGAACCAGCTTGAAGAATCTTAATCAGTTTCTTCCA	6540
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Db 6961 AATGCCTCAGCCAGATGA 6978

RESULT 2

AK074079

LOCUS AK074079 5804 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00150 protein.

ACCESSION AK074079

VERSION AK074079.1 GI:18676505

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE

2 (bases 1 to 5804)

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 76.7%; Score 5350.8; DB 5; Length 5804;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 5380; Conservative 0; Mismatches 2; Indels 18; Gaps 1;

Qy	1579	GCCGGAAGCAGAGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAA	1638
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Qy	1639	GACCCAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATT	1698
Db	61	GACCCAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATT	120
Qy	1699	ATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCT	1758
Db	121	ATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCT	180
Qy	1759	AAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCA	1818
Db	181	AAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCA	240
Qy	1819	AATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGCGGTGCAAGAATACCTGGGG	1878
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Qy	1879	ACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAA	1938
Db	301	ACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAA	360
Qy	1939	GAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGACCAGCTGGAAATAGTT	1998
Db	361	GAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGACCAGCTGGAAATAGTT	420
Qy	1999	GCCATGGATGCAGAAAATATGAGGAAGGAGCTTGAGAGCTAGAAAGTGCCCTCCAAGAG	2058
Db	421	GCCATGGATGCAGAAAATATGAGGAAGGAGCTTGAGAGCTAGAAAGTGCCCTCCAAGAG	480

Qy	2059	CAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCT	2118
Db	481	CAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCT	540
Qy	2119	GAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTG	2178
Db	541	GAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTG	600
Qy	2179	GAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAG	2238
Db	601	GAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAG	660
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Db	661	GAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAAGCCAGTTCTCAGAAGAAAAGGAGCAA	720
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Db	721	GAGAACAGTGAGCTCCATGCAAACTTAAACACTTGCAGGATGACAATAATCTGTTAAAA	780
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Db	781	CAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCCA	840
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Db	841	GAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAA	900
Qy	2479	ATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAA	2538
Db	901	ATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAA	960
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Qy	2719	GCAAGAAATCCAGCAAATGGAGAATGAAATTCATATTTGCAAGAAAATCTAAAAAGTATG	2778
Db	1141	GCAAGAAATCCAGCAAATGGAGAATGAAATTCATATTTGCAAGAAAATCTAAAAAGTATG	1200
Qy	2779	GAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAGGAGAGA	2838
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Qy	2839	ATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAG	2898
Db	1261	ATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAG	1320
Qy	2899	GAGCAAGTTTTTGGTTTGTAGATAAAGAACTGAAGAAAAGTAAAGAAAGCCGTGGCCACCTCT	2958
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Qy	2959	GATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGA	3018
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Qy	3019	ACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGC	3078
Db	1441	ACTGTTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGC	1500
Qy	3079	AGAAAGGCAGCACAAAGCAGCCAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTG	3138
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Qy	3139	CAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTA	3198
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Qy	3199	GGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAAACTGAATGAGACAATGGAACGA	3258
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Qy	3259	CAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAA	3318
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Qy	3319	GGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAG	3378
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Qy	3379	AATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATG	3438
Db	1801	AATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTACTTTATG	1860
Qy	3439	CCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGT	3498
Db	1861	CCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGT	1920
Qy	3499	GTTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAGCAGGAT	3558
Db	1921	GTTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAGCAGGAT	1980
Qy	3559	GGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGG	3618
Db	1981	GGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGG	2040
Qy	3619	AGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAA	3678
Db	2041	AGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAA	2100
Qy	3679	GAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATG	3738
Db	2101	GAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATG	2160
Qy	3739	TATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCT	3798
Db	2161	TATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCT	2220
Qy	3799	CCTCCCTTGCCAAACAATAGCCGACCTCTACCCCTGGCACTGTTGTTTATGGCCACCT	3858
Db	2221	CCTCCCTTGCCAAACAATAGCCGACCTCTACCCCTGGCACTGTTGTTTATGGCCACCT	2280
Qy	3859	CCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCACTTCTCCATCCCCTTCATC	3918

Db	2281	 CCTGCTGGGGCCCCC-----CCCCCAACTTCTCCATCCCCTTCATC	2322
Qy	3919	CCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCT	3978
Db	2323	 CCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCT	2382
Qy	3979	AGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGA	4038
Db	2383	 AGATTAGAAGACATAATGCAGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGA	2442
Qy	4039	GCATCCAAGCGGCAGTCGAGAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTT	4098
Db	2443	 GCATCCAAGCGGCAGTCGAGAGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTT	2502
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Db	2683	 ACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAG	2742
Qy	4339	AGTGAACTTTCATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCACTGATGCC	4398
Db	2743	 AGTGAACTTTCATGCACTAAAGAAAAGACAAAAAATGCTGTTGAAAAGTTCACTGATGCC	2802
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Db	2803	 AAGAGAAGTTTATTGCAAACTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAA	2862
Qy	4459	ACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAG	4518
Db	2863	 ACTGCTGTTAACCTCGTCAAAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAG	2922
Qy	4519	GATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTA	4578
Db	2923	 GATTTGGAGCAGCACAAAATCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTA	2982
Qy	4579	GCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAG	4638
Db	2983	 GCAGCAAAAGACTCAGACTTCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAG	3042
Qy	4639	CTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAG	4698
Db	3043	 CTTCAGAAACTACAGAAAGACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAG	3102
Qy	4699	GTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAA	4758
Db	3103	 GTCCTTAAAGAATCTGAGGTGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAA	3162
Qy	4759	AGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAA	4818

Db	3163	AGCCAGGTGACAAGTCAGCAGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAA	3222
Qy	4819	AAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAGCTGACCTCCAGGAA	4878
Db	3223	AAGGAGGAGCTGCATCTACTCCAAGGAAGCATGGTCCAGGCAAAGCTGACCTCCAGGAA	3282
Qy	4879	GCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAA	4938
Db	3283	GCTCTGAGACTGGGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAA	3342
Qy	4939	TCTCTTCTGGAAGAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGA	4998
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Qy	4999	AAAACCTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTT	5058
Db	3403	AAAACCTCAACTTACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAATCTTCAGGTT	3462
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Qy	5659	CTGCTTCACACCACCAAGCATCAGGATGTGTTGCTCAGTGAGCAGACCCGACTCCAGAAG	5718
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Qy	6559	GAAGCTATTTTGGAAAGAAAACGAAAACCTAGAAGGAGAATTGGAAAGCTTGAAAGAGAAC	6618
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Qy	6739	CGACTCAAGGCCCACTCCGACACTGTATGTCCAAGCAAGCAGAAGTATTAATTAAAGGA	6798
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Qy	6799	AAGCGGCAGACAGAGGGCACTTTACACAGTTTGAGGAGACAAGTAGATGCTTTAGGGGAA	6858
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Qy	6859	TTGGTCACCAGCACCTCTGCAGATTCAGCGTCATCACCCAGTCTGTCTCAGCTGGAGTCT	6918
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Qy	6919	TCCCTCACAGAGGACTCTCAACTTGGACAAAATCAGGAAAAGAATGCCTCAGCCAGATGA	6978
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RESULT 3

AY651261

LOCUS AY651261 3735 bp mRNA linear PRI 18-SEP-2005

DEFINITION Homo sapiens centrosomal protein 1 (CEP1) mRNA, partial cds.

ACCESSION AY651261

VERSION AY651261.1 GI:60686982

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3735)

AUTHORS Guinn,B.A., Bland,E.A., Lodi,U., Liggins,A.P., Tobal,K.,
Petters,S., Wells,J.W., Banham,A.H. and Mufti,G.J.

TITLE Humoral detection of leukaemia-associated antigens in presentation
acute myeloid leukaemia

JOURNAL Biochem. Biophys. Res. Commun. 335 (4), 1293-1304 (2005)

PUBMED 16112646

REFERENCE 2 (bases 1 to 3735)

AUTHORS Guinn,B.A., Bland,E.A. and Mufti,G.J.

TITLE Direct Submission

JOURNAL Submitted (11-JUN-2004) Department of Haematological Medicine,
Guy's, King's & St. Thomas' School of Medicine, 123 Coldharbour
Lane, London SE5 9NU, U.K.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 53.5%; Score 3735; DB 5; Length 3735;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1298	CACCACTGGACACGCAACTGGAAGACAAAGAAAAAAATAAGTGCAGCACAAACTCGAC	1357
Db	1	CACCACTGGACACGCAACTGGAAGACAAAGAAAAAAATAAGTGCAGCACAAACTCGAC	60
Qy	1358	TATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAACAATTTTGAGAGCTACTGAAG	1417
Db	61	TATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAACAATTTTGAGAGCTACTGAAG	120
Qy	1418	AATTTAAACAACTGGAAGAGCTATACAACTAAAAAAGATTTTCAGAAGCAGGGAAAGACC	1477
Db	121	AATTTAAACAACTGGAAGAGCTATACAACTAAAAAAGATTTTCAGAAGCAGGGAAAGACC	180
Qy	1478	TTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTGTAAATAAATTACGCCAGGAAGCTC	1537
Db	181	TTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTGTAAATAAATTACGCCAGGAAGCTC	240
Qy	1538	TGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGA	1597
Db	241	TGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGA	300
Qy	1598	TTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATA	1657
Db	301	TTAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATA	360
Qy	1658	TGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAAC	1717
Db	361	TGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAAC	420
Qy	1718	AACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTA	1777

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Db      421  |||...||| AACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTA 480
Qy      1778 AGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGG 1837
Db      481  |||...||| AGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGG 540
Qy      1838 ATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAA 1897
Db      541  |||...||| ATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAA 600
Qy      1898 CTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGAT 1957
Db      601  |||...||| CTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGAT 660
Qy      1958 TGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATA 2017
Db      661  |||...||| TGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATA 720
Qy      2018 TGAGGAAGGAGCTTGACAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCAT 2077
Db      721  |||...||| TGAGGAAGGAGCTTGACAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCAT 780
Qy      2078 CTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAA 2137
Db      781  |||...||| CTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAA 840
Qy      2138 ACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTA 2197
Db      841  |||...||| ACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTA 900
Qy      2198 CCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGA 2257
Db      901  |||...||| CCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGA 960
Qy      2258 ATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATG 2317
Db      961  |||...||| ATGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATG 1020
Qy      2318 CAAAACCTTAAACACTTGACAGGATGACAATAATCTGTTAAAACAGCAACTTAAAGATTTCC 2377
Db      1021 |||...||| CAAAACCTTAAACACTTGACAGGATGACAATAATCTGTTAAAACAGCAACTTAAAGATTTCC 1080
Qy      2378 AGAATCACCTTAACCATGTGGTTGATGGTTTGGTTTCGTCCAGAAGAAGTGGCAGCTCGTG 2437
Db      1081 |||...||| AGAATCACCTTAACCATGTGGTTGATGGTTTGGTTTCGTCCAGAAGAAGTGGCAGCTCGTG 1140
Qy      2438 TGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCTT 2497
Db      1141 |||...||| TGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCTT 1200
Qy      2498 CAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCTTGAC 2557
Db      1201 |||...||| CAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCTTGAC 1260
Qy      2558 GCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGG 2617
Db      1261 |||...||| GCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGG 1320
Qy      2618 CTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAG 2677
Db      |||...|||

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Db	1321	CTCTGCAGCAAGAGAACTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAG	1380
Qy	2678	CCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGG	2737
Db	1381	CCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGG	1440
Qy	2738	AGAATGAAATTCACATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTA	2797
Db	1441	AGAATGAAATTCACATTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTA	1500
Qy	2798	CAGATCTCCAACCTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAG	2857
Db	1501	CAGATCTCCAACCTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAG	1560
Qy	2858	AGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAG	2917
Db	1561	AGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAG	1620
Qy	2918	ATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTG	2977
Db	1621	ATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTG	1680
Qy	2978	AGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAACGTGTATGAAAATTAACC	3037
Db	1681	AGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAACGTGTATGAAAATTAACC	1740
Qy	3038	AGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCAG	3097
Db	1741	AGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCAG	1800
Qy	3098	CCAGAGATCTACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGA	3157
Db	1801	CCAGAGATCTACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGA	1860
Qy	3158	AGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCAC	3217
Db	1861	AGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCAC	1920
Qy	3218	AGGTCCTAGAAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCAA	3277
Db	1921	AGGTCCTAGAAAATTGAGAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCAA	1980
Qy	3278	GGCTGCAGAAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTT	3337
Db	1981	GGCTGCAGAAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTT	2040
Qy	3338	TAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCA	3397
Db	2041	TAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCA	2100
Qy	3398	TGGCAGATCCTTTCAAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCAA	3457
Db	2101	TGGCAGATCCTTTCAAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCAA	2160
Qy	3458	AAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAG	3517
Db	2161	AAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAG	2220
Qy	3518	CCTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAAC	3577
Db	2221	CCTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAAC	2280

Qy	3578	CTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGT	3637
Db	2281	CTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGT	2340
Qy	3638	TTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACC	3697
Db	2341	TTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACC	2400
Qy	3698	AAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATG	3757
Db	2401	AAGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATG	2460
Qy	3758	GTTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATA	3817
Db	2461	GTTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATA	2520
Qy	3818	GCCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGG	3877
Db	2521	GCCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGG	2580
Qy	3878	TGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATT	3937
Db	2581	TGTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATT	2640
Qy	3938	GCAACGTCCCTGAACACCATAAAGTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGC	3997
Db	2641	GCAACGTCCCTGAACACCATAAAGTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGC	2700
Qy	3998	AGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGG	4057
Db	2701	AGCATTTAAATCAAAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGG	2760
Qy	4058	AGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCT	4117
Db	2761	AGAAAGAAATGGAAGAACTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCT	2820
Qy	4118	TAGAGTGTGAAGTAGAAGAATTACATAGAAGTGTCCAGAAACGTCAACAGCAAAAGGACT	4177
Db	2821	TAGAGTGTGAAGTAGAAGAATTACATAGAAGTGTCCAGAAACGTCAACAGCAAAAGGACT	2880
Qy	4178	TCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAAC	4237
Db	2881	TCATTGATGGAAATGTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAAC	2940
Qy	4238	ATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCT	4297
Db	2941	ATCATGAAGATATTGTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCT	3000
Qy	4298	CAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACCTTCATGCACTA	4357
Db	3001	CAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACCTTCATGCACTA	3060
Qy	4358	AAGAAAAGACAAAAAATGCTGTTGAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAA	4417
Db	3061	AAGAAAAGACAAAAAATGCTGTTGAAAAGTTCACTGATGCCAAGAGAAGTTTATTGCAAA	3120
Qy	4418	CTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCA	4477
Db	3121	CTGAGTCAGATGCTGAGGAATTAGAAAGGAGAGCTCAGGAACTGCTGTTAACCTCGTCA	3180

Qy	4478	AAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAA	4537
Db	3181	AAGCTGATCAGCAGCTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAA	3240
Qy	4538	TCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACT	4597
Db	3241	TCAAGCAAGAAGAAATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACT	3300
Qy	4598	TCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAGCTTCAGAACTACAGAAAG	4657
Db	3301	TCCAATGTTTAAGCAAGAAGAAGGAAAACTGACAGAAGAGCTTCAGAACTACAGAAAG	3360
Qy	4658	ACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGG	4717
Db	3361	ACATAGAGATGGCAGAACGCAATGAGGATCACCACCTGCAGGTCCTTAAAGAATCTGAGG	3420
Qy	4718	TGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGC	4777
Db	3421	TGCTTCTTCAGGCCAAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGC	3480
Qy	4778	AGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTAC	4837
Db	3481	AGCAGGAGATGGCTGTCTTGGACAGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTAC	3540
Qy	4838	TCCAAGGAAGCATGGTCCAGGCAAAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGA	4897
Db	3541	TCCAAGGAAGCATGGTCCAGGCAAAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGA	3600
Qy	4898	CTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGA	4957
Db	3601	CTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAAATCTCTTCTGGAAGAACTGA	3660
Qy	4958	GTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTA	5017
Db	3661	GTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAACTTACACTTA	3720
Qy	5018	TAAAGCAGGAAATTG	5032
Db	3721	TAAAGCAGGAAATTG	3735

RESULT 4

CQ850900

LOCUS CQ850900 3602 bp DNA linear PAT 23-AUG-2004

DEFINITION Sequence 1369 from Patent EP1447413.

ACCESSION CQ850900

VERSION CQ850900.1 GI:51509112

KEYWORDS

SOURCE Homo sapiens (human).

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
 Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.

TITLE Full-length human cDNA

JOURNAL Patent: EP 1447413-A 1369 18-AUG-2004;
 Research Association for Biotechnology (JP)

FEATURES Location/Qualifiers

source 1. .3602

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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ORIGIN

Query Match 51.6%; Score 3597.4; DB 2; Length 3602;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      459 CTTATCATATAACAAAATCAGCAAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAA 518
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Db      4   CTTATCATATAACAAAATCAGCAAAATTGAAGGCATAGAAAATATGTGTAATCTGCAAAA 63

Qy      519 GCTTAACCTTGCAGGAAATGAAATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAA 578
        |||
Db      64   GCTTAACCTTGCAGGAAATGAAATTGAGCATATTCCAGTATGGTTAGGGAAGAAGTTAAA 123

Qy      579 ATCTTTGCGAGTCCTCAATTTGAAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAA 638
        |||
Db      124 ATCTTTGCGAGTCCTCAATTTGAAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAA 183

Qy      639 GTTGAAACCGCTTCAAGATTGATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCCT 698
        |||
Db      184 GTTGAAACTGCTTCAAGATTGATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCCT 243

Qy      699 TCCTCATTACCTCCAGTTTACCATTTTCCACCTCCGTTTCATTGGAAAGTTTGAAGGTCA 758
        |||
Db      244 TCCTCATTACCTCCAGTTTACCATTTTCCACCTCCGTTTCATTGGAAAGTTTGAAGGTCA 303

Qy      759 GCCAGTAACCACTCAGGATAGACAGGAGGCTTTTGAGAGATTCAGTTTAGAAGAGGTAGA 818
        |||
Db      304 GCCAGTAACCACTCAGGATAGACAGGAGGCTTTTGAGAGATTCAGTTTAGAAGAGGTAGA 363

Qy      819 AAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAAACTGAAGAGCTTAAGAGCAAACA 878
        |||
Db      364 AAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAAACTGAAGAGCTTAAGAGCAAACA 423

Qy      879 AACAAGGTTCCCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCATTAAGAGGA 938
        |||
Db      424 AACAAGGTTCCCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCATTAAGAGGA 483

Qy      939 GGCCATGTTACAGAAACAGAGCTGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGA 998
        |||
Db      484 GGCCATGTTACAGAAACAGAGCTGTGAGGAACTCAAGAGTGACTTAAACACAAAAAATGA 543

Qy      999 ATTGCTAAAACAGAAGACCATAGAATTAACACGAGCATGTCAGAAGCAATATGAGCTGGA 1058
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Qy      1059 ACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAATTATTATCCATC 1118
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Qy      1179 CAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGAT 1238
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Db      724 CAAGAGAAATATGTTTGCCACAGAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGAT 783

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Qy	1239	CAAGAAGATGGAGCCAGATGAACAACTTAGAAATGATCACATGAACTTGAGAGGCCACAC	1298
Db	784	CAAGAAGATGGAGCCAGATGAACAACTTAGAAATGATCACATGAACTTGAGAGGCCACAC	843
Qy	1299	ACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCACAACTCGACT	1358
Db	844	ACCACTGGACACGCAACTGGAAGACAAAGAAAAAAAAAATAAGTGCAGCACAACTCGACT	903
Qy	1359	ATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAAACAATTTTGAGAGCTACTGAAGA	1418
Db	904	ATCAGAACTGCATGATGAAATAGAAAAGGCAGAACAAACAATTTTGAGAGCTACTGAAGA	963
Qy	1419	ATTTAAACAACCTGGAAGAAGCTATACAACCTAAAAAGATTTTCAGAAGCAGGGAAAGACCT	1478
Db	964	ATTTAAACAACCTGGAAGAAGCTATACAACCTAAAAAGATTTTCAGAAGCAGGGAAAGACCT	1023
Qy	1479	TCTTTACAAGCAGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCT	1538
Db	1024	TCTTTACAAGCAGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCT	1083
Qy	1539	GGATCTAGAAGTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGAT	1598
Db	1084	GGATCTAGAAGTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGAT	1143
Qy	1599	TAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATAT	1658
Db	1144	TAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATAT	1203
Qy	1659	GAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAACA	1718
Db	1204	GAAGGCTCAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAACA	1263
Qy	1719	ACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAA	1778
Db	1264	ACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAA	1323
Qy	1779	GGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGA	1838
Db	1324	GGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGA	1383
Qy	1839	TTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAAC	1898
Db	1384	TTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAAC	1443
Qy	1899	TCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATT	1958
Db	1444	TCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGTTGCAGAGATT	1503
Qy	1959	GACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATAT	2018
Db	1504	GACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATAT	1563
Qy	2019	GAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATC	2078
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Qy	2079	TTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAA	2138
Db	1624	TTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAA	1683
Qy	2139	CCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTAC	2198

Db	1684		CCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTAC	1743
Qy	2199		CCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAA	2258
Db	1744		CCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAA	1803
Qy	2259		TGCCCTTGAAAAAGCCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGC	2318
Db	1804		TGCCCTTGAAAAAGCCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGC	1863
Qy	2319		AAAACCTTAAACACTTGCAGGATGACAATAATCTGTAAAACAGCAACTTAAAGATTTC	2378
Db	1864		AAAACCTTAAACACTTGCAGGATGACAATAATCTGTAAAACAGCAACTTAAAGATTTC	1923
Qy	2379		GAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCAGAGAAGTGGCAGCTCGTGT	2438
Db	1924		GAATCACCTTAACCATGTGGTTGATGGTTTGGTTCGTCAGAGAAGTGGCAGCTCGTGT	1983
Qy	2439		GGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCTTC	2498
Db	1984		GGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCTTC	2043
Qy	2499		AGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCCTGCACG	2558
Db	2044		AGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCCTGCACG	2103
Qy	2559		CTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGC	2618
Db	2104		CTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGC	2163
Qy	2619		TCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAGC	2678
Db	2164		TCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAGC	2223
Qy	2679		CCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGA	2738
Db	2224		CCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGA	2283
Qy	2739		GAATGAAATTCACATTTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTAC	2798
Db	2284		GAATGAAATTCACATTTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTAC	2343
Qy	2799		AGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGA	2858
Db	2344		AGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGA	2403
Qy	2859		GTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGA	2918
Db	2404		GTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGA	2463
Qy	2919		TAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGA	2978
Db	2464		TAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGA	2523
Qy	2979		GCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCA	3038
Db	2524		GCTCACCATTGCCAAAGACCAGCTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCA	2583
Qy	3039		GGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAGCAGC	3098

Db	2584	GGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTCAGCAGAAAGGCAGCACAAGCAGC	2643
Qy	3099	CAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAA	3158
Db	2644	CAGAGATCTCACCCGAGCAGAAGCTGAGATCGAACTCCTGCAGAATCTCCTCAGGCAGAA	2703
Qy	3159	GGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACA	3218
Db	2704	GGGGGAGCAGTTTCGACTTGAGATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACA	2763
Qy	3219	GGTCCTAGAAATTGAGAAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCAAG	3278
Db	2764	GGTCCTAGAAATTGAGAAACTGAATGAGACAATGGAACGACAAAGGACAGAGATTGCAAG	2823
Qy	3279	GCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTT	3338
Db	2824	GCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTT	2883
Qy	3339	AGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCAT	3398
Db	2884	AGAAGAAATTGCTGAACTTCGACGTGAAGTTTCTTATCAGAATGATTACATAAGCAGCAT	2943
Qy	3399	GGCAGATCCTTTCAAAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCAA	3458
Db	2944	GGCAGATCCTTTCAAAAAGACGAGGCTATTGGTACTTTATGCCACCACCACCATCATCAA	3003
Qy	3459	AGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGC	3518
Db	3004	AGTTTCCAGCCATAGTTCCCAGGCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGC	3063
Qy	3519	CTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACC	3578
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Db	3124	TCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTTACATAAACTGTT	3183
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Db	3244	AGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGG	3303
Qy	3759	TTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAG	3818
Db	3304	TTCTCCTGTACCCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAG	3363
Qy	3819	CCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGT	3878
Db	3364	CCGACCTCTCACCCCTGGCACTGTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGT	3423
Qy	3879	GTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTG	3938
Db	3424	GTATGGGCCTCCACCCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTG	3483
Qy	3939	CAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCA	3998
Db	3484	CAACGTCCCTGAACACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCA	3543

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RESULT 5

AK128098

LOCUS AK128098 3602 bp mRNA linear PRI 20-JAN-2006

DEFINITION Homo sapiens cDNA FLJ46219 fis, clone TESTI4013742, moderately similar to Mus musculus antigen identified by monoclonal antibody 2A8 (Ma2a8).

ACCESSION AK128098

VERSION AK128098.1 GI:34535302

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3602)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

FEATURES

source

Location/Qualifiers

1. .3602

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/tissue_type="testis"

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CDS

47. .>3602

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ORIGIN

Query Match 51.6%; Score 3597.4; DB 5; Length 3602;
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Qy	579	ATCTTTGCGAGTCCTCAATTTGAAAGGCAACAAGATATCATCGCTCCAAGATATAAGCAA	638
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Qy	639	GTTGAAACCGCTTCAAGATTGATTTCTCTGATCCTAGTTGAAAATCCAGTTGTGACCCCT	698
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Qy	759	GCCAGTAACCACTCAGGATAGACAGGAGGCTTTTGAGAGATTAGTTTAGAAGAGGTAGA	818
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Qy	819	AAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACA	878
Db	364	AAGACTGGAAAGAGACCTAGAAAAAAGATGATAGAACTGAAGAGCTTAAGAGCAAACA	423
Qy	879	AACAAGGTTCCCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGA	938
Db	424	AACAAGGTTCCCTTGAGGAAATTAAAAATCAAGATAAATTGAATAAATCATTAAAAGAGGA	483
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Qy	1059	ACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAATTATTATCCATC	1118
Db	604	ACAGGAATTGGCCTTTTATAAAATTGATGCTAAATTTGAGCCACTAAATTATTATCCATC	663
Qy	1119	AGAGTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATA	1178
Db	664	AGAGTATGCTGAAATTGATAAAGCCCCAGATGAAAGCCCTTACATTGGCAAATCCAGATA	723
Qy	1179	CAAGAGAAATATGTTTGGCCACAGAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGAT	1238
Db	724	CAAGAGAAATATGTTTGGCCACAGAGAGTTATATTATTGACAGTGCTCAGGCAGTACAGAT	783
Qy	1239	CAAGAAGATGGAGCCAGATGAACAACTTAGAAATGATCACATGAACTTGAGAGGCCACAC	1298
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Qy	1419	ATTTAAACAACTGGAAGAAGCTATACAACCTAAAAAGATTTTTCAGAAGCAGGGAAAGACCT	1478
Db	964	ATTTAAACAACTGGAAGAAGCTATACAACCTAAAAAGATTTTTCAGAAGCAGGGAAAGACCT	1023
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Db	1024	TCTTTACAAGCAGTTGAGTGGTAGACTACAACCTTGTAATAAATTACGCCAGGAAGCTCT	1083
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Db	1084	GGATCTAGAACTGCAGATGGAAAAGCAAAAGCAGGAAATTGCCGGAAGCAGAAGGAGAT	1143
Qy	1599	TAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATAT	1658
Db	1144	TAAGGACCTGCAAATAGCCATAGATAGCCTGGATTCCAAAGACCCAAAACATTCCCATAT	1203
Qy	1659	GAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAACA	1718
Db	1204	GAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGCAGTACCAACA	1263
Qy	1719	ACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAA	1778
Db	1264	ACTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGGAAGAGATTAA	1323
Qy	1779	GGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGA	1838
Db	1324	GGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCCTGAAGAAGGA	1383
Qy	1839	TTTAGAAGGTGTTATCAGTGGGTTGCAAGAATACCTGGGGACCATTAAAGGCCAGGCAAC	1898
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Qy	1959	GACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATAT	2018
Db	1504	GACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATGCAGAAAATAT	1563
Qy	2019	GAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATC	2078
Db	1564	GAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGGTGAATGCATC	1623
Qy	2079	TTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAA	2138
Db	1624	TTTGCAGCAGACCCAGGGAGATCTCAGTGCCTATGAAGCTGAGCTAGAGGCTCGGCTAAA	1683
Qy	2139	CCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTAC	2198
Db	1684	CCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAAGAGTTGGAAAAAGTAACAAGACTTAC	1743
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Db	1744	CCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAGCCCTCAAGAA	1803
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Db	1804	TGCCCTTGGAAGGCCAGTTCTCAGAAGAAAAGGAGCAAGAGAACAGTGAGCTCCATGC	1863
Qy	2319	AAACTTAAACACTTGCAGGATGACAATAATCTGTTAAACAGCAACTTAAAGATTTCCA	2378
Db	1864	AAACTTAAACACTTGCAGGATGACAATAATCTGTTAAACAGCAACTTAAAGATTTCCA	1923
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Qy	2439	GGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCCTTC	2498
Db	1984	GGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCCATAGTCCCTTC	2043
Qy	2499	AGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCTTGACAG	2558
Db	2044	AGATGTCTTAGGGAAAAGTCTTGCTGATTTACAGAAACAATTCAGTGAAATTCTTGACAG	2103
Qy	2559	CTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGAGAGAGAAAAGTCCAAGAAGAAATGGC	2618
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Db	2164	TCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTCAGGCAGGCCTGTGAGAGAGC	2223
Qy	2679	CCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGA	2738
Db	2224	CCTGGAAGCAAGAATGAATTTTGATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGA	2283
Qy	2739	GAATGAAATTCACATTTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTAC	2798
Db	2284	GAATGAAATTCACATTTTGCAAGAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTAC	2343
Qy	2799	AGATCTCCAACCTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGA	2858

Db	2344	 AGATCTCCAACCTTCAGGAAGCTGATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGA	2403
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Db	2404	 GTTAGAGAAAAAGAAGAACTTGAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGA	2463
Qy	2919	TAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGA	2978
Db	2464	 TAAAGAACTGAAGAACTAAAGAAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGA	2523
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Db	2584	 GGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGGTTTCAGCAGAAAGGCAGCACAAAGCAGC	2643
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Qy	3279	GCTGCAGAATGTACTAGACCTCACTGGAAGTGACAACAAAGGAGGCTTTGAAAATGTTTT	3338
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Db	3064	 CTCAACTCCTGTTAGAAAACACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACC	3123
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Db	3124	 TCCCCCTGCCTCAGGATACTGGGTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTT	3183
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Db      3244 AGAAGAACCCCCATTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGG 3303
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Db      3304 TTCTCCTGTACCCAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAG 3363
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RESULT 6

AF083322

LOCUS AF083322 3893 bp mRNA linear PRI 20-AUG-1998

DEFINITION Homo sapiens centriole associated protein CEP110 mRNA, complete cds.

ACCESSION AF083322

VERSION AF083322.1 GI:3435243

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3893)

AUTHORS Mack,G.J., Fritzler,M.J. and Rattner,J.B.

TITLE Cep110, a novel protein of the centriole identified with human autoimmune sera

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3893)

AUTHORS Mack,G.J., Fritzler,M.J. and Rattner,J.B.

TITLE Direct Submission

JOURNAL Submitted (24-JUL-1998) Medical Biochemistry, University of Calgary, 3330 Hospital Dr. NW, Calgary, AB T2N4N1, Canada

FEATURES Location/Qualifiers

source 1..3893
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ORIGIN

Query Match 43.1%; Score 3008.6; DB 5; Length 3893;
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 Matches 3011; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 7

CQ724459

LOCUS CQ724459 3882 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 10393 from Patent WO02068579.

ACCESSION CQ724459

VERSION CQ724459.1 GI:42285316

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

JOURNAL Patent: WO 02068579-A 10393 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES
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ORIGIN

Query Match 43.0%; Score 3000.8; DB 2; Length 3882;
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RESULT 8

BC002932

LOCUS BC002932 3037 bp mRNA linear PRI 09-FEB-2006

DEFINITION Homo sapiens centrosomal protein 110kDa, mRNA (cDNA clone IMAGE:3956474), partial cds.

ACCESSION BC002932

VERSION BC002932.2 GI:33877372

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3037)

AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 3037)

AUTHORS .

CONSRTM NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT On Aug 19, 2003 this sequence version replaced gi:13937655.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 15 Row: i Column: 20.

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source Location/Qualifiers

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ORIGIN

Query Match 41.4%; Score 2890.2; DB 5; Length 3037;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 9

CS168804

LOCUS CS168804 3044 bp DNA linear PAT 05-OCT-2005

DEFINITION Sequence 2049 from Patent EP1580263.

ACCESSION CS168804

VERSION CS168804.1 GI:77155917

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T.

TITLE Full-length cDNA sequences

JOURNAL Patent: EP 1580263-A 2049 28-SEP-2005;

Research Association for Biotech nology (JP)

FEATURES

source

Location/Qualifiers

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ORIGIN

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Qy      1813 GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATAC 1872
          |||
Db      721  GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATAC 780

Qy      1873 CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT 1932
          |||

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Db	781	CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	840
Qy	1933	GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	1992
Db	841	GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	900
Qy	1993	ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTC	2052
Db	901	ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTC	960
Qy	2053	CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	2112
Db	961	CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	1020
Qy	2113	GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	2172
Db	1021	GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	1080
Qy	2173	GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	2232
Db	1081	GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	1140
Qy	2233	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGCCAGTTCTCAGAAGAAAAAG	2292
Db	1141	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGGAAGCCAGTTCTCAGAAGAAAAAG	1200
Qy	2293	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGACAATAATCTG	2352
Db	1201	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGACAATAATCTG	1260
Qy	2353	TTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	2412
Db	1261	TTAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	1320
Qy	2413	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACT	2472
Db	1321	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACT	1380
Qy	2473	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAG	2532
Db	1381	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTTACAG	1440
Qy	2533	AAACAATTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGA	2592
Db	1441	AAACAATTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAGTTAGA	1500
Qy	2593	GAGAGAAAAGTCCAAGAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAA	2652
Db	1501	GAGAGAAAAGTCCAAGAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAA	1560
Qy	2653	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	2712
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Qy	2713	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	2772
Db	1621	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	1680
Qy	2773	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAG	2832
Db	1681	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAG	1740

Qy	2833	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	2892
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Qy	2893	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCC	2952
Db	1801	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAGAAAGCCGTGGCC	1860
Qy	2953	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	3012
Db	1861	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	1920
Qy	3013	CATGGAACGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	3072
Db	1921	CATGGAACGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	1980
Qy	3073	TTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAA	3132
Db	1981	TTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAA	2040
Qy	3133	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	3192
Db	2041	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	2100
Qy	3193	GGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	3252
Db	2101	GGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	2160
Qy	3253	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	3312
Db	2161	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	2220
Qy	3313	AACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCT	3372
Db	2221	AACAAAGGAGGCTTTGAAAATGTTTTAGAAAGAAATTGCTGAACTTCGACGTGAAGTTTCT	2280
Qy	3373	TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC	3432
Db	2281	TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC	2340
Qy	3433	TTTATGCCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGAC	3492
Db	2341	TTTATGCCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGAC	2400
Qy	3493	TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAG	3552
Db	2401	TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCACGCCCTGGGCAG	2460
Qy	3553	CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC	3612
Db	2461	CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC	2520
Qy	3613	ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT	3672
Db	2521	ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT	2580
Qy	3673	CAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCTGGATAC	3732
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Qy      3733 ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA 3792
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Qy      3793 CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTACCCCTGGCACTGTTGTTTATGGC 3852
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Db      2701 CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTACCCCTGGCACTGTTGTTTATGGC 2760

Qy      3853 CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCC 3912
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Db      2761 CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCC 2820

Qy      3913 TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAA 3972
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Db      2821 TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGTAAGTGA 2880

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RESULT 10

AX834925

LOCUS AX834925 3044 bp DNA linear PAT 15-DEC-2003

DEFINITION Sequence 2049 from Patent EP1347046.

ACCESSION AX834925

VERSION AX834925.1 GI:39921060

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.

TITLE Full-length cDNA sequences

JOURNAL Patent: EP 1347046-A 2049 24-SEP-2003;
Research Association for Biotechnology (JP)

FEATURES Location/Qualifiers

source 1. .3044
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 41.2%; Score 2873.6; DB 2; Length 3044;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2876; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1093 TTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAA 1152
          |||
Db      1   TTTGAGCCACTAAATTATTATCCATCAGAGTATGCTGAAATTGATAAAGCCCCAGATGAA 60

Qy      1153 AGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATT 1212
          |||
Db      61   AGCCCTTACATTGGCAAATCCAGATACAAGAGAAATATGTTTGCCACAGAGAGTTATATT 120

Qy      1213 ATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACTTAGAAAT 1272
          |||
Db      121 ATTGACAGTGCTCAGGCAGTACAGATCAAGAAGATGGAGCCAGATGAACAACTTAGAAAT 180

Qy      1273 GATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAA 1332

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Db	181	 GATCACATGAACTTGAGAGGCCACACACCACTGGACACGCAACTGGAAGACAAAGAAAAA	240
Qy	1333	AAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAA	1392
Db	241	 AAAATAAGTGCAGCACAACTCGACTATCAGAACTGCATGATGAAATAGAAAAGGCAGAA	300
Qy	1393	CAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACTAAAA	1452
Db	301	 CAACAAATTTTGAGAGCTACTGAAGAATTTAAACAACCTGGAAGAAGCTATACAACTAAAA	360
Qy	1453	AAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTT	1512
Db	361	 AAGATTTTCAGAAGCAGGGAAAGACCTTCTTTACAAGCAGTTGAGTGGTAGACTACAACCTT	420
Qy	1513	GTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAG	1572
Db	421	 GTAAATAAATTACGCCAGGAAGCTCTGGATCTAGAACTGCAGATGGAAAAGCAAAAGCAG	480
Qy	1573	GAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGAT	1632
Db	481	 GAAATTGCCGGAAGCAGAAGGAGATTAAGGACCTGCAAATAGCCATAGATAGCCTGGAT	540
Qy	1633	TCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTT	1692
Db	541	 TCCAAAGACCCAAAACATTCCCATATGAAGGCTCAAAGAGCGGTAAAGAACAACAGCTT	600
Qy	1693	GACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGA	1752
Db	601	 GACATTATGAACAAGCAGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGA	660
Qy	1753	ATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATA	1812
Db	661	 ATTGCTAAGGAAACGGAAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATA	720
Qy	1813	GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATAC	1872
Db	721	 GCAGCAAATGAAGCCCTGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTTGCAAGAATAC	780
Qy	1873	CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	1932
Db	781	 CTGGGGACCATTAAAGGCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGAT	840
Qy	1933	GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGACCAGCTGGAA	1992
Db	841	 GAGAAAGAGACATTGTTGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAA	900
Qy	1993	ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGAGAGCTAGAAAGTGCCCTC	2052
Db	901	 ATAGTTGCCATGGATGCAGAAAATATGAGGAAGGAGCTTGAGAGCTAGAAAGTGCCCTC	960
Qy	2053	CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	2112
Db	961	 CAAGAGCAGCATGAGGTGAATGCATCTTTGCAGCAGACCCAGGGAGATCTCAGTGCCTAT	1020
Qy	2113	GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	2172
Db	1021	 GAAGCTGAGCTAGAGGCTCGGCTAAACCTAAGGGATGCTGAAGCCAACCAGCTCAAGGAA	1080
Qy	2173	GAGTTGGAAGAAAGTAACAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTT	2232

Db	1081	GAGTTGGAAAAAGTAACAAGACTTACCCAGTTAGAACAAATCAGCCCTTCAAGCAGAACTT	1140
Qy	2233	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAGCCCAGTTCTCAGAAGAAAAAG	2292
Db	1141	GAGAAGGAAAGGCAAGCCCTCAAGAATGCCCTTGAAAAGCCCAGTTCTCAGAAGAAAAAG	1200
Qy	2293	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGACAATAATCTG	2352
Db	1201	GAGCAAGAGAACAGTGAGCTCCATGCAAAACTTAAACACTTGCAGGATGACAATAATCTG	1260
Qy	2353	TTAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	2412
Db	1261	TTAAAACAGCAACTTAAAGATTTCCAGAATCACCTTAACCATGTGGTTGATGGTTTGGTT	1320
Qy	2413	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACT	2472
Db	1321	CGTCCAGAAGAAGTGGCAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACT	1380
Qy	2473	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTACAG	2532
Db	1381	GGGGAAATGAACATCCATAGTCCTTCAGATGTCTTAGGGAAAAGTCTTGCTGATTACAG	1440
Qy	2533	AAACAATTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGA	2592
Db	1441	AAACAATTCAGTGAAATTCTTGACGCTCCAAGTGGGAAAGAGATGAAGCACAAAGTTAGA	1500
Qy	2593	GAGAGAAAAGTCCAAGAAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAA	2652
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Qy	2653	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	2712
Db	1561	GAGTTCAGGCAGGCCTGTGAGAGAGCCCTGGAAGCAAGAATGAATTTTGATAAGAGGCAA	1620
Qy	2713	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	2772
Db	1621	CATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTGCAAGAAAATCTAAAA	1680
Qy	2773	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAG	2832
Db	1681	AGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAAGTTCAGGAAGCTGATGAAGAGAAG	1740
Qy	2833	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	2892
Db	1741	GAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTTGAAGATGCCAAA	1800
Qy	2893	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAAGTGAAGAACTAAAGAAAGCCGTGGCC	2952
Db	1801	TCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAAGTGAAGAACTAAAGAAAGCCGTGGCC	1860
Qy	2953	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	3012
Db	1861	ACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAGCTGAAGTCCCTT	1920
Qy	3013	CATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	3072
Db	1921	CATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAGGAAGCAGAGAGG	1980
Qy	3073	TTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAA	3132
Db	1981	TTCAGCAGAAAGGCAGCACAAAGCAGCCAGAGATCTACCCGAGCAGAAGCTGAGATCGAA	2040

Qy	3133	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	3192
Db	2041	CTCCTGCAGAATCTCCTCAGGCAGAAGGGGGAGCAGTTTCGACTTGAGATGGAGAAAACA	2100
Qy	3193	GGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	3252
Db	2101	GGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTGAATGAGACAATG	2160
Qy	3253	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	3312
Db	2161	GAACGACAAAGGACAGAGATTGCAAGGCTGCAGAATGTACTAGACCTCACTGGAAGTGAC	2220
Qy	3313	AACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCT	3372
Db	2221	AACAAAGGAGGCTTTGAAAATGTTTTAGAAGAAATTGCTGAACTTCGACGTGAAGTTTCT	2280
Qy	3373	TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC	3432
Db	2281	TATCAGAATGATTACATAAGCAGCATGGCAGATCCTTTCAAAGACGAGGCTATTGGTAC	2340
Qy	3433	TTTATGCCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGAC	3492
Db	2341	TTTATGCCACCACCACCATCATCAAAAGTTTCCAGCCATAGTTCCCAGGCCACCAAGGAC	2400
Qy	3493	TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACACGCCCTGGGCAG	3552
Db	2401	TCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACACGCCCTGGGCAG	2460
Qy	3553	CAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGGGTTTATTCTCCC	3612
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Qy	3613	ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT	3672
Db	2521	ATCAGGAGTGGGTTACATAAACTGTTTCCAAGTAGAGATGCAGACAGTGGAGGAGATAGT	2580
Qy	3673	CAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCATTTGTGCCTCCTCTGGATAC	3732
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Qy	3733	ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA	3792
Db	2641	ATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCCAGGGCATGGCCCTGTATGCA	2700
Qy	3793	CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGC	3852
Db	2701	CCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACTGTTGTTTATGGC	2760
Qy	3853	CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCC	3912
Db	2761	CCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCCAACTTCTCCATCCCC	2820
Qy	3913	TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGAGAATGAA	3972
Db	2821	TTCATCCCTATGGGTGTGCTGCATTGCAACGTCCCTGAACACCATAACTTAGTAAGTGA	2880

RESULT 11

AK097636

LOCUS

AK097636

3044 bp

mRNA

linear

PRI 20-JAN-2006

DEFINITION Homo sapiens cDNA FLJ40317 fis, clone TESTI2030554, moderately similar to M.musculus mRNA for IB3/5-polypeptide.
ACCESSION AK097636
VERSION AK097636.1 GI:21757469
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T.O., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039
REFERENCE 2
AUTHORS Kanehori,K., Ishibashi,T., Chiba,Y., Fujimori,K., Hiraoka,S., Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 3044)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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 Best Local Similarity 99.9%; Pred. No. 0;
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RESULT 12

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DEFINITION Homo sapiens centrosomal protein 110kDa, mRNA (cDNA clone IMAGE:4123463).

ACCESSION BC009287

VERSION BC009287.2 GI:39644860

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 2803)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2803)
 AUTHORS .
 CONSRTM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Dec 9, 2003 this sequence version replaced gi:14627275.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
 Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
 Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
 McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
 Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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ORIGIN

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Db	2041	CGTCGCTCAGAGCTCAGGGAAGCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTTCA	2100
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Db	2581	CATCTACTCCAAGGAAGCATGGTCCAGGCAAAAGCTGACCTCCAGGAAGCTCTGAGACTG	2640
Qy	4891	GGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAATCTCTTCTGGAA	4950
Db	2641	GGAGAGACTGAAGTAACTGAGAAGTGCAATCACATTAGGGAAGTAAATCTCTTCTGGAA	2700
Qy	4951	GAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAACTT	5010
Db	2701	GAACTGAGTTTTTCAGAAAGGAGAACTAAATGTTTCAGATTAGTGAAAGAAAACTCAACTT	2760
Qy	5011	ACACTTATAAAGCAGGAAATTGAAAAAGAGGAAGAAAA	5048
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RESULT 13

AK131139

LOCUS AK131139 3974 bp mRNA linear ROD 01-MAR-2005

DEFINITION Mus musculus mRNA for mFLJ00150 protein.

ACCESSION AK131139

VERSION AK131139.1 GI:47847433

KEYWORDS FLI_CDNA.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Koseki,H., Hiraoka,S.,
Saga,Y., Kitamura,H., Nakagawa,T., Nagase,T., Ohara,O. and Koga,H.

TITLE Prediction of the Coding Sequences of Mouse Homologues of FLJ
Genes: The Complete Nucleotide Sequences of 110 Mouse
FLJ-Homologous cDNAs Identified by Screening of Terminal Sequences
of cDNA Clones Randomly Sampled from Size-Fractionated Libraries

JOURNAL DNA Res. 11, 167-180 (2004)

REFERENCE 2 (bases 1 to 3974)

AUTHORS Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.

TITLE Direct Submission

JOURNAL Submitted (04-FEB-2004) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)

COMMENT The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.

FEATURES Location/Qualifiers

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/db_xref="taxon:10090"
/clone="mfj11357"
/tissue_type="fetal brain"
/note="vector:modified pBC SK+"

gene

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/gene="mFLJ00150"

CDS

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/gene="mFLJ00150"
/inference="non-experimental evidence, no additional
details recorded"
/note="CDS is predicted by in silico analysis. Start codon
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ORIGIN

Query Match 34.5%; Score 2410.4; DB 6; Length 3974;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 2805; Conservative 0; Mismatches 636; Indels 3; Gaps 1;

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Qy	3532	AGAAAACCACGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCA	3591
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Qy	3592	GGATACTGGGTTTATTCTCCCATCAGGAGTGGGTACATAAACTGTTTCCAAGTAGAGAT	3651
Db	121	GGGTACTGGGTCTACTCCCCCATCAGAAGCACGCTGCATAAGTCATTTTCAAAGAGAGAT	180
Qy	3652	GCAGACAGTGGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCCA	3711
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Qy	3712	TTTGTGCCTCCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCC	3771
Db	241	TTTGTGCCTCCCCCTGGGTACATAATGTATACTGTACTTCCTGATGGTTCTCCTGTACCC	300
Qy	3772	CAGGGCATGGCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACC	3831
Db	301	CAGGGAGTGGCCCTGTATGCACCATCGCCTCCATTGCCCAACAGCAGCCATCCTCTGACC	360
Qy	3832	CCTGGCACTGTTGTTTATGGCCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCA	3891
Db	361	CCCGGCACTGTGTTTATGGGCCACCTCCTGCTGGGGCCCCCATCATATACGGACCTCCT	420
Qy	3892	CCCCCAACTTCTCCATCCCCTTCATCCCTATGGGTGTGCTGCATTGCAACGTCCTGAA	3951
Db	421	CCTGCCAACTTCGCTGTTCCCCTTGTCCTCCGCGGGTGTGCAGCATTGCAACATCCCAGAG	480
Qy	3952	CACCATAACTTAGAGAATGAAGTTTCTAGATTAGAAGACATAATGCAGCATTAAATCA	4011
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Qy	4012	AAGAAGCGGGAAGAAAGGTGGATGAGAGCATCCAAGCGGCAGTCGGAGAAAGAAATGGAA	4071
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Qy	4072	GAAGTGCATCATAATATTGATGATCTTTTGCAAGAGAAGAAAAGCTTAGAGTGTGAAGTA	4131
Db	601	GGGCTGCACCGTGATATTGATGACCTTTTGCAAGAGAAGAAAAGTAACTTGAAGTA	660

Qy	4132	GAAGAATTACATAGAACTGTCCAGAAACGTCACACAGCAAAAGGACTTCATTGATGGAAAT	4191
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Qy	4192	GTTGAGAGTCTTATGACTGAACTAGAAATAGAAAAATCACTCAAACATCATGAAGATATT	4251
Db	721	GTTGAGAATCTTATGACTGAACTAGAAATAGAAAAAGTCTCTCAAACATCATGAGGATATC	780
Qy	4252	GTAGATGAAATTGAGTGCATTGAGAAGACTCTTCTGAAACGTCGCTCAGAGCTCAGGGAA	4311
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Qy	4312	GCTGACCGACTCCTGGCAGAGGCTGAGAGTGAACTTTCATGCACTAAAGAAAAGACAAAA	4371
Db	841	GCTGACCGACTCTCTGGCGGAAGCCGAGAATGAGCTTGCATGCACCAAGGAGAAGACAAAG	900
Qy	4372	AATGCTGTTGAAAAGTTCAGTATGCCAAGAGAAGTTTATTGCAAACAGTGCAGATGCT	4431
Db	901	AGTGCTGTTGAAAATTCAGTATGCCAAGAGAAATTTATTACAAACCGAGTCAGACGCT	960
Qy	4432	GAGGAATTAGAAAAGGAGAGCTCAGGAACTGCTGTAAACCTCGTCAAAGCTGATCAGCAG	4491
Db	961	GAGGCACTAGAAAAGAGAGCCAGGAGACTGCACTTAACCTTGTGAAAGCAGAGCAGCAG	1020
Qy	4492	CTAAGATCGCTCCAGGCTGATGCAAAGGATTTGGAGCAGCACAAAATCAAGCAAGAAGAA	4551
Db	1021	CTAAGACTGCTCCAGGCTGATGCAGAGGACTTGGAGCAGCACAAAATCAAACAAGAAGAA	1080
Qy	4552	ATCTTGAAAGAAATAAACAAAATTGTAGCAGCAAAAGACTCAGACTTCCAATGTTTAAGC	4611
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Qy	4612	AAGAAGAAGGAAAAACTGACAGAAGAGCTTCAGAACTACAGAAAGACATAGAGATGGCA	4671
Db	1141	GAGAAGAAGGAAAAACTGACAGAAGAGCTTCAGAGTCTGCAGAGAGACATCAAGGCAGCG	1200
Qy	4672	GAACGCAATGAGGATCACACCTGCAGGTCTTAAAGAATCTGAGGTGCTTCTTCAGGCC	4731
Db	1201	CAACACAGTGAGGATCACACCTTCAGGTCTTAGAGAGTCTGAGACTCTCCTTCAGGCC	1260
Qy	4732	AAAAGAGCCGAGCTGGAAAAGCTGAAAAGCCAGGTGACAAGTCAGCAGCAGGAGATGGCT	4791
Db	1261	AAGAGAGCTGAGCTGGAAACACTGAAAAGCCAGGTGACAAGCCAGCAGCAGGAGTTGGCT	1320
Qy	4792	GTCTTGACAGGCAGTTAGGGCATAAAAAGGAGGAGCTGCATCTACTCCAAGGAAGCATG	4851
Db	1321	GTCTTGAGCTCAGAGTTGGGGCATAGAAGGGAGGAGCTGCTTCTACTCCAGGACAGCCTC	1380
Qy	4852	GTCCAGGC AAAAGCTGACCTCCAGGAAGCTCTGAGACTGGGAGAGACTGAAGTAACTGAG	4911
Db	1381	GCCCAGGC AAAAGCTGACCTCCAGGAAGCCCTGACACTGGGGGAGACGGAAGTTGCTGAG	1440
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Db	1441	AAGTGCAATCACATTAGGGAAGTAAATCACTTCTTGGAAGAACTAAGTTTTTCAGAAAGGA	1500
Qy	4972	GAACTAAATGTTTCAAGATTAGTGAAGAAAACTCAACTTACACTTATAAAGCAGGAAATT	5031
Db	1501	GAACTGAATGTCCACATCAGTGAAAAGAAGACTCAGCTCGCACTTATACAGCAGGAGATG	1560
Qy	5032	GAAAAAGAGGAAGAAAATCTTCAGGTTGTTTTAAGGCAGATGTCTAAACATAAAACCGAA	5091

Db	1561	GAGAAAGAGGAAAAGAATCTTCAGGTGGTTTACAGCAGCTGTCGAGACATAAGACTGAA	1620
Qy	5092	CTAAAGAATATTCTGGACATGTTGCAACTTGAAAACCATGAGCTACAAGGTTTGAAGCTA	5151
Db	1621	CTAAAGAATGTTGCAGACATACTGCAGCTTGAAACCAGCGAGCTCCAAGGTCTGAAGCTC	1680
Qy	5152	CAACATGACCAAAGGGTATCTGAATTAGAGAAGACTCAGGTGGCAGTGCTAGAGGAGAAA	5211
Db	1681	CAGCATGACCAGAAGGTGGTGGAGCTGGAGAAGGCGCAGGTGGACGTGCTGGAGGAGAAA	1740
Qy	5212	CTGGAGTTAGAGAATTTGCAGCAGATATCCAGCAGCAGAAAAGGGGAAATAGAGTGGCAG	5271
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Qy	5272	AAGCAGCTCCTTGAGAGGGATAAACGAGAAATAGAACGAATGACTGCTGAGTCCCGAGCT	5331
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Qy	5332	TTACAATCGTGTGTTGAGTGTGTTGAGCAAAGAAAAGGAAGATCTCCAAGAGAAATGTGAC	5391
Db	1861	CTGCAGTCCTGCGTCGAATGTCTGAGTAAAGAAAAGGAGGATCTCCAAGGACAGTGCGAG	1920
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Qy	5572	CAGCTCCAAGAAAAACGAGAAGCAGTAAACTCACTGCAGGAGGAACTAGCTAATGTCCAA	5631
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Qy	5692	CTCAGTGAGCAGACCCGACTCCAGAAGGACATCAGTGAATGGGCAAATAGTTTGAAGAC	5751
Db	2221	CTCAATGAGCAGACGCAGCTGCAGGAGGACATCAGCAAATGGATGGCCAGGTAGAGAGC	2280
Qy	5752	TGTCAGAAAGAAGAGGAGACAAAACAACAACAACTTCAAGTGCTTCAAGTGAAGATTGAA	5811
Db	2281	TGCCAGAAAGAGACGGAGACAAAGGAACAGCAAGTCCAGCAGCTCCAGGATGAGATCAGA	2340
Qy	5812	GAAAACAAGCTCAAACCTAGTCCAACAAGAAATGATGTTTCAGAGACTCCAGAAAGAGAGA	5871
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Db	2521	GCAGCTGAAGGACGCCTGGGAACCTGCAGGAAGAGGAGCGGCGCATTGAGGGCCTGGAG	2580
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Db	2641	TCAGGTGAGCTGCTGGCCCTGCAGAAAGAGGCTGACGATATGAGGGCCGACTTCAGCCTC	2700
Qy	6172	CTGCGGAACCAGTTCTTGACAGAAAGAAAGAAAGCTGAGAAGCAGGTGGCCAGCCTGAAG	6231
Db	2701	CTGAGGAACCAGTTCTTAACAGAAAGGAAGAAGGCAGAGAAGCAGGTGGCCGGCTAAAG	2760
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Qy	6412	AAACAGATGGCAAACCAAAAAGATTTGGAGAGAAGACAAATGGAAATCAGTGATGCAATG	6471
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Qy	6532	TTTCTTCCAGAACTACCAGCAGATCTAGAAGCTATTTTGGAAAGAAACGAAAACCTAGAA	6591
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Qy	6592	GGAGAATTGGAAAGCTTGAAAGAGAACCTTCCATTTACCATGAATGAGGGACCTTTTGAA	6651
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Qy	6832	AGGAGACAAGTAGATGCTTTAGGGGAATTGGTCAACCAGCACCTCTGCAGATTACGCGTCA	6891
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 Db 3418 TCACCCAGTCTGCCTTCCCTTGTG 3441

RESULT 14

AR717552

LOCUS AR717552 2631 bp DNA linear PAT 07-OCT-2005

DEFINITION Sequence 52 from patent US 6943241.

ACCESSION AR717552

VERSION AR717552.1 GI:77366506

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2631)

AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
 Yamamoto,J.-i., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
 Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
 Masuho,Y.

TITLE Full-length cDNA

JOURNAL Patent: US 6943241-A 52 13-SEP-2005;
 Research Association for Biotechnology; Tokyo;
 WOX;

FEATURES Location/Qualifiers
 source 1. .2631
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ORIGIN

Query Match 34.4%; Score 2403.2; DB 2; Length 2631;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 2446; Conservative 0; Mismatches 8; Indels 28; Gaps 1;

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 Db 330 TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATACCTGGGGACCATTAAAG 389

Qy 1889 GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT 1948
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 Db 450 TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG 509

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Qy	2429	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCC	2488
Db	930	CAGCTCGTGTGGATGAGCTAAGAAGAAAAGTGAATTAGGAACTGGGGAAATGAACATCC	989
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Qy	2701	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACTATTTGCAA	2760
Db	1230	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACTATTTGCAA	1289
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAAATCCAAGGCCTTACAGATCTCCAACCTTCAGGAAGCT	2820
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Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
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Qy	3181	ATGGAGAAAACAGGTGTAGGTACTGGAGCAAACCTCACAGGTCCTAGAAAATTGAGAAACTG	3240
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Qy	3661	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCATTTGTGCCT	3720
Db	2190	GGAGGAGATAGTCAGGAAGAGAGTGAGCTGGATGACCAAGAAGAACCCCATTTGTGCCT	2249
Qy	3721	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCAGGGCATG	3780
Db	2250	CCTCCTGGATACATGATGTATACTGTGCTTCCTGATGGTTCTCCTGTACCCAGGGCATG	2309
Qy	3781	GCCCTGTATGCACCACCTCCTCCCTTGCCAAACAATAGCCGACCTCTCACCCCTGGCACT	3840
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RESULT 15

AX746527

LOCUS AX746527 2631 bp mRNA linear PAT 20-JUN-2003

DEFINITION Sequence 52 from Patent EP1308459.

ACCESSION AX746527

VERSION AX746527.1 GI:32130794

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.

TITLE Full-length cDNA sequences

JOURNAL Patent: EP 1308459-A 52 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)

FEATURES

source Location/Qualifiers
1. .2631
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/mol_type="mRNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 34.4%; Score 2403.2; DB 2; Length 2631;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2446; Conservative 0; Mismatches 8; Indels 28; Gaps 1;

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Db      150 AGTCCCATATGAAGGCTCAAAAGAGCGGTAAAGAACAACAGCTTGACATTATGAACAAGC 209

Qy      1709 AGTACCAACAACCTTGAAAGTCGTTTGGATGAGATACTTTCTAGAATTGCTAAGGAAACGG 1768
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Db      210 AGTACCAACAACCTTGAAAGTCGTTTGGAGGAGATACTTTCTAGAATTGCTAAGGAAACGG 269

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Qy	1769	AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC	1828
Db	270	AAGAGATTAAGGACCTTGAAGAACAGCTTACTGAAGGCCAGATAGCAGCAAATGAAGCCC	329
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Db	330	TGAAGAAGGATTTAGAAGGTGTTATCAGTGGGTGCAAGAATACCTGGGGACCATTAAAG	389
Qy	1889	GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT	1948
Db	390	GCCAGGCAACTCAGGCCCAGAATGAGTGCAGGAAGCTGCGGGATGAGAAAGAGACATTGT	449
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Db	450	TGCAGAGATTGACAGAAGTCGAGCAGGAGAGAGACCAGCTGGAAATAGTTGCCATGGATG	509
Qy	2009	CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG	2068
Db	510	CAGAAAATATGAGGAAGGAGCTTGCAGAGCTAGAAAGTGCCCTCCAAGAGCAGCATGAGG	569
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Qy	2189	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	2248
Db	690	CAAGACTTACCCAGTTAGAACAATCAGCCCTTCAAGCAGAACTTGAGAAGGAAAGGCAAG	749
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Qy	2609	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTACGGCAGGCCCT	2668
Db	1110	AAGAAATGGCTCTGCAGCAAGAGAAAAGTGGCAACTGGACAAGAAGAGTTACGGCAGGCCCT	1169
Qy	2669	GTGAGAGAGCCCTGGAAGCAAGA-----ATGAATTTT	2700

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Db	1230	GATAAGAGGCAACATGAAGCAAGAATCCAGCAAATGGAGAATGAAATTCACATTTTGCAA	1289
Qy	2761	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCT	2820
Db	1290	GAAAATCTAAAAAGTATGGAGGAAATCCAAGGCCTTACAGATCTCCAACCTCAGGAAGCT	1349
Qy	2821	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	2880
Db	1350	GATGAAGAGAAGGAGAGAATTCTGGCCCAACTCCGAGAGTTAGAGAAAAAGAAGAACTT	1409
Qy	2881	GAAGATGCCAAATCTCAGGAGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	2940
Db	1410	GAAGATGCCAAATCTCAGGGCAAGTTTTTGGTTTAGATAAAGAACTGAAGAACTAAAG	1469
Qy	2941	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	3000
Db	1470	AAAGCCGTGGCCACCTCTGATAAGCTAGCCACAGCTGAGCTCACCATTGCCAAAGACCAG	1529
Qy	3001	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	3060
Db	1530	CTGAAGTCCCTTCATGGAAGTGTATGAAAATTAACCAGGAGCGAGCAGAGGAGTTGCAG	1589
Qy	3061	GAAGCAGAGAGGTTTACGAGAAAAGGCAGCACAAGCAGCCAGAGATCTCACCCGAGCAGAA	3120
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Qy	3181	ATGGAGAAAACAGGTGTAGTACTGGAGCAAACCTCACAGGTCCTAGAAATTGAGAACTG	3240
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Db	1950	GGCTATTGGTACTTTATGCCACCACCACCATCATCAAAGTTTCCAGCCATAGTTCCCAG	2009
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Db	2010	GCCACCAAGGACTCTGGTGTGGCCTTAAGTACTCAGCCTCAACTCCTGTTAGAAAACCA	2069
Qy	3541	CGCCCTGGGCAGCAGGATGGGAAGGAAGGCAGTCAACCTCCCCCTGCCTCAGGATACTGG	3600

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Db      2370 GTTGTTTATGGCCACCTCCTGCTGGGGCCCCCATGGTGTATGGGCCTCCACCCCCAAC 2429
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